

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 29, 2005, 18:47:48 ; Search time 1178 Seconds
(without alignments)
19529.306 Million cell updates/sec

Title: US-10-613-728-1

Perfect score: 5735
Sequence: 1 ggaatcctggaaggtcacaca.....cataagagttcagtcgac 5735

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	534.4	9.3	613	8	AZ269661 RPCI-23-4
C 2	499.4	8.7	529	8	BH073204 RPCI-24-3
C 3	473.8	8.3	496	8	AZ300332 RPCI-23-1
C 4	305.6	5.3	312	8	AZ457684 IM0261E12
C 5	305.2	5.3	469	8	BH285252 CH230-118
C 6	266.4	4.6	447	8	AZ729312 RPCI-24-7
C 7	236	4.1	447	5	BY000251 BY000251
C 8	225.2	3.9	616	2	BF525096 UI-R-AC0-
C 9	145.4	2.5	370	8	AZ407663 IM0178C01
C 10	133.4	2.3	390	5	BY000731 BY000731
C 11	133.4	2.3	409	5	BY061731 BY061731
C 12	133.4	2.3	415	5	BY083328 BY083328
C 13	133.4	2.3	739	6	CB596657 AGENCOURT
C 14	133.4	2.3	741	6	CB599099 AGENCOURT
C 15	133.4	2.3	783	6	CA490238 AGENCOURT
C 16	133.4	2.3	843	6	CA460851 AGENCOURT
C 17	133.4	2.3	843	6	CA495692 AGENCOURT
C 18	133.4	2.3	850	6	CA490440 AGENCOURT
C 19	133.4	2.3	917	6	CA490678 AGENCOURT
C 20	133.4	2.3	920	6	CA490677 AGENCOURT
C 21	132.8	2.3	871	6	CA490555 AGENCOURT
C 22	132.4	2.3	363	5	BY083663 BY083663
C 23	131.8	2.3	881	6	CB951696 CB951696
C 24	130	2.3	253	5	BX632021 BX632021

C 25	130	2.3	459	1	AI642327
C 26	129.6	2.3	378	5	BY064144
C 27	129.2	2.3	224	5	BY000659
C 28	129	2.2	707	1	AA855323
C 29	127	2.2	349	1	AI892571
C 30	126.8	2.2	412	5	BY435020
C 31	126.8	2.2	468	5	BY414811
C 32	126.2	2.2	243	5	BY000397
C 33	125.2	2.2	368	2	BF472804
C 34	125.2	2.2	385	5	BY422659
C 35	125.2	2.2	428	5	BF462620
C 36	124.8	2.2	399	5	BY432934
C 37	123.8	2.2	405	5	BY419314
C 38	123.8	2.2	425	5	BY427154
C 39	123.6	2.2	405	5	BY436012
C 40	123	2.1	426	1	AA140343
C 41	123	2.1	473	1	AA919406
C 42	122.8	2.1	203	5	BY426544
C 43	122.8	2.1	246	1	AV244652
C 44	122.8	2.1	278	4	BM124558
C 45	122.8	2.1	313	5	BY415619

ALIGNMENTS

RESULT 1
LOCUS A2269661/c 613 bp DNA linear GSS 26-JUL-2000
DEFINITION RPCI-23-444F20.TV RPCI-23 Mus musculus genomic clone
A2269661
RPCI-23-444F20, genomic survey sequence.

ACCESSION A2269661
VERSION A2269661.1 GI:9483276
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatman,S.,
1 (bases 1 to 613)
Aktiret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-444F20.TV

TITLE JOURNAL
COMMENT
Contact: Shaying Zhao
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Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Library are derived from the mouse BAC library RPCI-23. For BAC
clones availability, please contact Piter de Jong
(piter@dejong.med.buflalo.edu). Clones may be purchased from
BACPRAC Resources (http://bacpac.med.buflalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/cdb/bac/ends/mouse/bac_end_intro.html
Place: 444 row: F column: 20
Seq primer: SP6
Class: BAC ends.

FEATURES

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Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-444F20"
/sex="Female"
/lab_host="DH10B"
/clone_11b="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACet.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or

DEFINITION RPCI-23-117N22.TV RPCI-23 Mus musculus genomic clone
 RPCI-23-117N22, genomic survey sequence.
 ACCESSION AZ300332
 VERSION AZ300332.1 GI:9542117
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
 1 (bases 1 to 496)
 Zhao, S., Nierman, W., Felblyum, T., Malek, J., Shatsman, S.,
 Akiner, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de
 Jong, P. and Fraser, C. M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other_GSSs: RPCI-23-117N22.TV
 Contact: Shaying Zhao
 Department of Bukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieterdejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
 or from Resea ch Genetics (info@resgen.com). BAC end page:
 http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
 Plate: 117 row: N column: 22
 Seq primer: SP6
 Class: BAC ends.

FEATURES
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 Location/Qualifiers
 1..496
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-117N22"
 /sex="Female"
 /lab_host="DH10B"
 /clone_lib="RPCI-23"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
 EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBACe3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN
 Query Match 8.3%; Score 473.8; DB 8; Length 496;
 Best Local Similarity 98.4%; Pred. No. 7.1e-114;
 Matches 489; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 3259 CCACACTTAACTCTTCTCCCTCAGCCCAAGTTAAACCTTGCCCTTCCCTCCG 3318
 |||||
 DB 496 CCACACTTAACTCTTCTCCCTCAGCCCAAGTTAAACCTTGCCCTTCCCTCCG 437
 |||||

QY 3319 ACCTCCCATCAGAGTGAAGGTTGCAAGAGGAGGTTAAACCTTACATGTCACATC 3378
 |||||
 DB 436 ACCTCCCATCAGAGTGAAGGTTGCAAGAGGAGGTTAAACCTTACATGTCACATC 377
 |||||

QY 3379 ATGTGACAGATATATGATCAGTATGTGTAAGGCAAGAAATCTGCAGGCTTAA 3438
 |||||
 DB 376 ATGTGACAGATATATGATCAGTATGTGTAAGGCAAGAAATCTGCAGGCTTAA 318
 |||||

QY 3439 CTGGGTTAATGTGTAAGTCTGTGTCAGTGTGTGCTGCTGAAGAAACGGGCAATGC 3498
 |||||
 DB 317 CTGGGTTAATGTGTAAGTCTGTGTCAGTGTGTGCTGCTGAAGAAACGGGCAATGC 258
 |||||

QY 3499 TGTGACAGCTGTTGCTGTGTGCTGAGGTTACAGACTGCAGGTTGTGTGTAATTGC 3558
 |||||

DB 257 TGTGACAGCTGTTCACTTCTGTGTCGTGAGGTTACAGACTGCAGGTTGTGTGTAATTGC 198
 |||||

QY 3559 CCAAGGCAAAAGTGGTGAATCCCTTCCATGTGTTAAAGATGTGATGATGCGCTGCATC 3618
 |||||

DB 197 CCAAGGCAAAAGTGGTGAATCCCTTCCATGTGTTAAAGATGTGATGATGCGCTGCATC 138
 |||||

QY 3619 TCAGGACCATGAAATATGAAATGAGACACTTATATGTGTCTCTTAAGCTTAAGTGAAG 3678
 |||||

DB 137 TCAGGACCATGAAATATGAAATGAGACACTTATATGTGTCTCTTAAGCTTAAGTGAAG 78
 |||||

QY 3679 GTCTTTGAGAGACACCTGCTCTAGATGTGGCAACAGACTACAGACATGATCTGTAC 3738
 |||||

DB 77 GTCTTTGAGAGACACCTGCTCTAGATGTGGCAACAGACTACAGACATGATCTGTAC 18
 |||||

QY 3739 AGAGTTAAGAGAGAGAG 3755
 |||||

DB 17 AGAGTTAAGAGAGAGAG 1
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RESULT 4
 AZ457684 312 bp DNA linear GSS 04-OCT-2000
 LOCUS
 DEFINITION IM0261B12F Mouse 10kb plasmid UGCLM library Mus musculus genomic
 clone UGCLM0261B12 F, genomic survey sequence.
 ACCESSION AZ457684
 VERSION AZ457684.1 GI:10615809
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
 1 (bases 1 to 312)
 Dunn, D., Moyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0261 row: E column: 12
 Seq primer: CGTGTGTAAGACAGCGCCAGT
 Class: Plasmid ends
 High quality sequence stop: 312.

FEATURES
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 Location/Qualifiers
 1..312
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLM0261B12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCLM library"
 /note="Vector: PMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male); Was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Napovor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|473114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 5.3%; Score 305.6; DB 8; Length 312;
Best Local Similarity 98.7%; Pred. No. 2.8e-69;
Matches 308; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 605 GTCTGGGGGTGTAAGAACTGACAGTACTTTTCAGTGGGAAAGTATGACCCCTCAG 664
DB 312 GTCTGGGGGTGTAAGAACTGACAGTACTTTTCAGTGGGAAAGTATGACCCCTCAG 253
QY 665 CAGATGTAGTATGTCCCTTATGATCCCATCCAGGAGGTCTCTAAGAGACATGGGAT 724
DB 252 CAGATGTAGTATGTCCCTTATGATCCCATCCAGGAGGTCTCTAAGAGACATGGGAT 193
QY 725 GAGAGATGTAGTATGTGAGATTCGCAACAGATATCCAGATGCCCTTGGCCCTTCC 764
DB 192 GAGAGATGTAGTATGTGAGATTCGCAACAGATATCCAGATGCCCTTGGCCCTTCC 133
QY 785 ACTTAGCAGAGAGACAGTAACTTAGCTTATCTTCTCCCTCCATCCCTCCAGACA 844
DB 132 ACTTAGCAGAGAGACAGTAACTTAGCTTATCTTCTCCCTCCATCCCTCCAGACA 73
QY 845 CACCCCTGCTGTCAGTATTCATTTCTTCTTCAAGTCCCTCTGTGACTTCATTTCG 904
DB 72 CACCCCTGCTGTCAGTATTCATTTCTTCTTCAAGTCCCTCTGTGACTTCATTTCG 13
QY 905 AAGGCTTTTAC 916
DB 12 AAGGCTTTTAC 1

RESULT 5 469 bp DNA linear GSS 30-NOV-2001
LOCUS BH285252
DEFINITION CH230-118C1, genomic survey sequence.
ACCESSION BH285252
VERSION BH285252.1 GI:17197658
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 469)
AUTHORS Zhao, S., Shetty, J., Shatsman, S., Teegay, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Rigg, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
OTHER GSS: CH230-118C1.TVB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Fax: 301 838 0208
Email: szhao@igr.org
Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ordering information.htm). BAC end page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html
Plate: 118 row: C column: 1

Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
FEATURES
source 1..469
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SENHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-118C1"
/sex="Female"
/cell_type="Brain"
/clone_11b="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SENHsd/MCW) BAC library produced by Pieter de Jong"

ORIGIN

Query Match 5.3%; Score 305.2; DB 8; Length 469;
Best Local Similarity 89.2%; Pred. No. 4.2e-69;
Matches 387; Conservative 0; Mismatches 38; Indels 9; Gaps 5;

QY 3787 GGAACCTGAGTGTGACCTGCAAGTGTGCTCCCTAGACATCATGACTTGTCTC 3846
DB 2 GGAACCTGAGTGTGACCTGCAAGTGTGCTCCCTAGACATCATGACTTGTCTC 61
QY 3847 TGGGAGCCAGCAGCTGTGAACTTCAAGTCTGAGAGTGAAGGCTCCCTCAGCTGA 3906
DB 62 TGGGAGCCAGCAGCTGTGAACTTCAAGTCTGAGAGTGAAGGCTCCCTCAGCTGA 119
QY 3907 AGCTATGCAATATGCCAGGTTGAAA--GGGGAAGGAGAGCTGTGATGGAGCTTGT 3964
DB 120 AGCTATGCAATATGCCAGGTTGAAA--GGGGAAGGAGAGCTGTGATGGAGCTTGT 179
QY 3965 GTGTGAGAGAGGAGGAGATTTAAGCTGGAAGAGAGGCTTTAGCCAGT--TG 4023
DB 180 GTGTGAGAGAGGAGGAGATTTAAGCTGGAAGAGAGGCTTTAGCCAGT--TG 229
QY 4024 TTCACTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 4080
DB 240 TTCACTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 299
QY 4081 GTGTGAGAGCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4140
DB 300 GTGTGAGAGCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 359
QY 4141 GCCCAAGACTAAAAAAGGCGATGAGCCAGAGGGGCGAAGCAACAGCTTTATGG 4200
DB 360 GCCCAAGACTAAAAAAGGCGCTGAGCCAGAGGGGCGAAGCAACAGCTTT--ATGG 418
QY 4201 GCAACCTTGGGCGC 4214
DB 419 GCAACCTTGAAGC 432

RESULT 6 447 bp DNA linear GSS 25-JAN-2001
LOCUS AZ729312
DEFINITION RPCI-24-79L13, TVB RPCI-24 Mus musculus genomic clone RPCI-24-79L13, genomic survey sequence.
ACCESSION AZ729312
VERSION AZ729312.1 GI:12486941
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 447)
AUTHORS Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akintet, B., Levins, M., Teegay, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999)
Contact: Shaying Zhao

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhoet@igrr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Piere de Jong (pdejong@igrr.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderingframe.html>). BAC end page: http://www.chori.org/tdb/bac_ends/mouse/bac_intro.html. Plate: 79 row: 1 column: 13
Seq primer: T7
Class: BAC ends.

FEATURES

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-79113"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: PTARBAC1; Site 1: BamHI; Site 2: BamHI; RPCI-24 Mouse BAC Library produced by Piere de Jong. The library was cloned in the PTARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

ORIGIN

Query Match 4.6%; Score 266.4; DB 8; Length 447;
Best Local Similarity 97.6%; Pred. No. 8.3e-59;
Matches 281; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 1 GGATCCCTGCAAGGTACACAGAGGCTCCACCCAGAGGCTCCTAGTCAATTCAGT 60
DB 161 GATTCCTGCAAGG-CATACATGATGCTCCACCCAGAGGCTCCTAGTCAATTCAGT 219
QY 61 TTCATGCTCTGTTCTCAACATGCTGCGCTCCCAAGAGCTAATTTGACTTTGTTTAT 120
DB 220 TTCATGCTCTGTTCTCAACATGCTGCGCTCCCAAGAGCTAATTTGACTTTGTTTAT 279
QY 121 TTCAAAGGCGCTGATAGAGAGTATGCTGCTACCCAGCTCTAAGGTCGCCGTA 180
DB 280 TTCAAAGGCGCTGATAGAGAGTATGCTGCTACCCAGCTCTAAGGTCGCCGTA 339
QY 181 AGCCCTCAGACCTGAGGCTTTGCAACAGCCCTTTAGTGAAGAGAAATTAAGCAATT 240
DB 340 AGCCCTCAGACCTGAGGCTTTGCAACAGCCCTTTAGTGAAGAGAAATTAAGCAATT 399
QY 241 TCCTTAAGCAAAATCTGCTCTAGACTCTTCTCTGACCTGCG 288
DB 400 TCCTTAAGCAAAATCTGCTCTAGACTCTTCTCTGACCTGCG 447

RESULT 7

BY000251 447 bp mRNA linear EST 06-DEC-2002
LOCUS BY000251 RIKEN full-length enriched, adult male heart Mus musculus
DEFINITION cDNA clone 1020001103 5', mRNA sequence.
ACCESSION BY000251
VERSION BY000251.1 GI:26060500

KEYWORDS

Mus musculus (house mouse)
EST.
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 447)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamana, K.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

JOURNAL MEDLINE PUBLISHED

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chorchi, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Matsui, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Nunata, K., Okido, T., Pavani, M.J., Pereira, G., Peckol, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wyszewski, B., Yang, I.,
Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterson, R., Lander, E.S.,
Rogers, J., Birney, E., and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watanishi, A., Watanabe, M., and
Hayashizaki, Y. Direct Submersion
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multichipillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse cDNAs.
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

FEATURES

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AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinsley, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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FEATURES

source

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was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD22 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE

AUTHORS

BY000731 390 bp mRNA linear EST 06-DEC-2002
BY000731 RIKEN full-length enriched, adult male heart Mus musculus
cDNA clone 1020031303 5', mRNA sequence.

BY000731.1 GI:26060980
EST.

1 (bases 1 to 390)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gotohori, T., Schiml, L.M., Kanapin, A., Matsuda, H.,
Hume, D.A., Quackenbush, J., Schiml, L.M., Kanapin, A., Matsuda, H.,
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Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimond, S.,
Gustincich, S., Hirokawa, N., Jackson, J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedziarski, R.M., King, B.L., Konagaya, A.,
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Maltais, L., Marchionni, L., McKenzie, D., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Petrea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,
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Wells, C., Wilming, L.G., Wyszynski, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
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Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Nunakawa, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
source

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1.390
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/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGCGCCCACTCGAGTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGATCCAGAGCTCAATTAATTAATTAACCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBlueScript KS(+) after bulk excision from Lambda FLC I."

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ORIGIN

Query Match 2.3%; Score 133.4; DB 5; Length 390;

Best Local Similarity 95.8%; Pred. No. 1.7e-23; Matches 137; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5289 TCCTGTCAGAGATCTAGATGTGTCCTCCAGCCTCTGCTACCTCTCTGCTGCTTC 5348

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RESULT 11

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LOCUS BY061731 409 bp mRNA linear EST 06-DEC-2002

DEFINITION BY061731 RIKEN full-length enriched, pooled tissues, 16 days

ACCESSION BY061731

VERSION BY061731.1 GI:26181469

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 409)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, T., Otsu, N., Saito, R., Suzuki, H., Yamana, K. I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bull, C.,

Hume, D. A., Quackenbush, J., Schriml, L. M., Kanpin, A., Matsuda, H.,

Batalov, S., Beisel, K. W., Blake, J. A., Brady, D., Brusic, V.,

Chotha, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,

Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,

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Guatiboldi, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,

Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongaya, A.,

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TITLE

JOURNAL
MEDLINE
PUBMED

COMMENT

Numata, K., Okido, T., Pavan, M. J., Perlea, G., Resole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
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Wells, C., Wilting, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
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Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
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Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
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Nature 420, 563-573 (2002)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
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10 (11), 1757-1771 (2000)
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encyclopedia: real-time sequence clustering for construction of a
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Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES
source

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ORIGIN

Query Match 2.3%; Score 133.4; DB 5; Length 409;

Best Local Similarity 95.8%; Pred. No. 1.7e-23;

Matches 137; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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Location/Qualifiers

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3' adaptors were used in cloning as follows:
5'-AAGCAGTGATACAGCGGCGGCGGCGG-3' and
5'-ATTCTAGAGCGGCGGCGGCGGCGGCGG-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC library."

ORIGIN

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VERSION CB599099.1 GI:29516955
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SOURCE Mus musculus (house mouse)

ORGANISM
Mus musculus

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AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 741)
TITLE NIH-MGC <http://mgs.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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Location/Qualifiers

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made by oligo-dt priming and directionally cloned. 5' and
3' adaptors were used in cloning as follows:
5'-AAGCAGTGATACAGCGGCGGCGGCGGCGG-3' and
5'-ATTCTAGAGCGGCGGCGGCGGCGGCGG-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC library."

ORIGIN

Query Match 2.3%; Score 133.4; DB 6; Length 741;
Best Local Similarity 95.8%; Pred. No. 2.1e-23;
Matches 137; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5289 TCCTGTGATGATCTAGATTGGTCTCCAGCCTCTGCTACTCTCTGCTGCTTC 5348
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QY 5349 CTCCTCTGTTCAGCTGCGCACTGTGTGCTCTGCTTCAGCTGTGTCACATTTCTCA 5408
|||
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Db 137 GGATTTCTGAAAGTTAACCAAG 159

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DEFINITION AGENCOURT 10825991 NIH_MGC 156 Mus musculus CDNA clone
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VERSION CA490238.1 GI:24953042
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 783)
TITLE NIH-MGC <http://mgs.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Bradfield Laboratory
CDNA Library Preparation: Mark Bltinger
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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Location/Qualifiers

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Dh 661 TCAGCAGATGTAATGTCTCCCTTGAATCCCATCCAGGAGGTCTCTAAGAGACATG 720
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Db 4501 CCACTCCCTATCACTGATATAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCACTGAT 4560
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Db 4561 AAGAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620
Qy 4621 TATGATGATGAT 4680
Db 4621 TATGATGATGAT 4680
Qy 4681 GGTATGATGAT 4740
Db 4681 GGTATGATGAT 4740
Qy 4741 GGAATGATGAT 4800
Db 4741 GGAATGATGAT 4800
Qy 4801 CCACTGATGAT 4860
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RESULT 2
US-10-024-066-5
; Sequence 5, Application US/10024066
; Publication No. US2002016134A1
; GENERAL INFORMATION:
; APPLICANT: Field, Loren J.
; TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
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; LENGTH: 5443
; TYPE: DNA
; ORGANISM: Mus musculus
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Query Match 88.0%; Score 5045; DB 13; Length 5443;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 5383; Conservative 0; Mismatches 60; Indels 292; Gaps 1;
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Db 1 GGAATGATGAT 60
Qy 61 TTCTGATGAT 120
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Db	481	GAAACAGGATTTAGAGAAAGCCTGACCTGACCTGAAAGCTCATCACAAGCA	540
Qy	541	AGCATCTAGGTGACCATGTAGTTAGTATCCTAGCGTGAATATATGACAGCTGGGCGAC	600
Db	541	AGCATCTAGGTGACCATGTAGTTAGTATCCTAGCGTGAATATATGACAGCTGGGCGAC	600
Qy	601	AGAAGTCCCTGGGGGTGTAGGAACCTGACCAAGTACCTTTTCAAGTCCGGCAAAAGTATACCCCC	660
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Qy	661	TCAGCAGATGATGATTAATGTCCCTTAGATCCCATCCAGGAGGGCTCTTAAGAGGACATG	720
Db	661	TCAGCAGATGATGATTAATGTCCCTTAGATCCCATCCAGGAGGGCTCTTAAGAGGACATG	720
Qy	721	GGATGAGAGATGTATGTCAATGTGGCATTTCCAAACACAGCTATCCACAGTGTCCCTTGCCCC	780
Db	721	GGATGAGAGATGTATGTCAATGTGGCATTTCCAAACACAGCTATCCACAGTGTCCCTTGCCCC	780
Qy	781	TTTCCACTTAAACAGAGGACAGTAACTTTAGCCTATCTTTCTCTCCCATCCGAC	840
Db	781	TTTCCACTTAAACAGAGGACAGTAACTTTAGCCTATCTTTCTCTCCCATCCGAC	840
Qy	841	GACACACCCCTGAGTCTGACAGTATTCATTTCTTCCCTTCAAGTCCCTCTGTGACTTCCAT	900
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Qy	901	TTTGAAGGCTTTTACCTGTGACAGTGTGTGAAGATTAAGTTTGGCCCTTAGGTGTGGCA	960
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Db	1021	TCACTGGCGGGCCTGGGGGTGTGAAAAAAGATGATGATGTCCGCTCCAGTAAAGCAAGC	1080
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Db	1081	TAGTCCCGCGAATATCTGTGCGACACAGCTGGGGTGTGGCTGGGGGTAAAGTATGTGGGTC	1140
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Qy	1201	ACACTCGGTGTGGCCACAGACTCTCTGTTCACAAGGCCCTCTGTGTCTGACCACTAGAGCTAG	1260
Db	1201	ACACTCGGTGTGGCCACAGACTCTCTGTTCACAAGGCCCTCTGTGTCTGACCACTAGAGCTAG	1260
Qy	1261	GCAACCAAGAGCATGGGCCCTGTGTGTGAGGATGGAAGATGTGTTTACCAATACCAAAAAACAG	1320
Db	1261	GCAACCAAGAGCATGGGCCCTGTGTGTGAGGATGGAAGATGTGTTTACCAATACCAAAAAACAG	1320
Qy	1321	CAGGGGAGGGAGAAACAAGAACGAATTAAGAGGAGAAAGAAAGGCCAGTCAATCAGA	1380
Db	1321	CAGGGGAGGGAGAAACAAGAACGAATTAAGAGGAGAAAGAAAGGCCAGTCAATCAGA	1380
Qy	1381	TGCAAGTCAAGAGAGATGGGAAGCCACAACAAGCTTGTGACAGAGAAACAAAAAGGGAG	1440
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Db	1621	GCAACTTAAGAGCCGAGAGCCTTAATAAGAGCAAGATTAAGTCTTCAAAAGTGGCCAG	1680
QY	1681	CTGTGCACACAGAGGGTGCAGAGACTGGTGGTAGACCTCAAGATTAAGATGATGCTCAGA	1740
Db	1681	CTGTGCACACAGAGGGTGCAGAGACTGGTGGTAGACCTCAAGATTAAGATGATGCTCAGA	1740
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Db	1741	ATGGGCGGGGGGGGGGATTTCTGGGGGGGGGAGAGAAAGGTGAAGAGAGCTGGAAACAG	1800
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Db	1801	AGAACTCTGGAAGCCCTGGAAACGATTAACATTAAGGAGAAACCCAGGCTACTTTAGATG	1860
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Db	1861	TAAATCATGAAAGACAGGGAGAGGGAAGCTGAGAGAGTGAAGAGACCCCGGGGCAAGA	1920
QY	1921	CATGGAAAGCAAGGACAAGGCCAGTTTGAGCCGCTCCGTAAATACACCTGCTGAAGGACAG	1980
Db	1921	CATGGAAAGCAAGGACAAGGCCAGTTTGAGCCGCTCCGTAAATACACCTGCTGAAGGACAG	1980
QY	1981	CCCTGTGATGAGCACCAGAACAGGAGAGCTTAAGGGTTAATGTCCAGA CAGGGAA CAGAG	2040
Db	1981	CCCTGTGATGAGCACCAGAACAGGAGAGCTTAAGGGTTAATGTCCAGA CAGGGAA CAGAG	2040
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Db	2041	GTAGA CACAGGAACAGACAGAGCGGGGAGCCAGGTAA CAAAGGAATGGTCTTCTCAC	2100
QY	2101	CTGTGGCCAGAGCGTCCATCTGTGTCCA CATACTCTTGAAATGTTCACTCAGCTGACGGC	2160
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QY	2161	TGGCTTGGGAAGGAGCTGGAAAGATATGTGAGAGCCAGGGGAGACAAGGGGGGCTTGA	2220
Db	2161	TGGCTTGGGAAGGAGCTGGAAAGATATGTGAGAGCCAGGGGAGACAAGGGGGGCTTGA	2220
QY	2221	AAGGAAGAGAGGGCCAAC CAGGCCACACACAAGAGGGCAGAGCC CAGACTGAATTA CTC	2280
Db	2221	AAGGAAGAGAGGGCCAAC CAGGCCACACACAAGAGGGCAGAGCC CAGACTGAATTA CTC	2280
QY	2281	CTTCTCTGTGCACTCTTCATAGAGAGCGATGGGA CTCTGTGACACCATCCCCATGA	2340
Db	2281	CTTCTCTGTGCACTCTTCATAGAGAGCGATGGGA CTCTGTGACACCATCCCCATGA	2340
QY	2341	GCCCCCACTACCAATCCAAAGTTTGGGCTGAGTGGCA TTTCAAGGTTCCCTGAGGACAG	2400
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QY	2401	CCTGGACCTTGTCTCTTGAAGCTTGACCCAAAGCTGACCCCAATGTTCTCAGTACCTTTGAA	2460
Db	2401	CCTGGACCTTGTCTCTTGAAGCTTGACCCAAAGCTGACCCCAATGTTCTCAGTACCTTTGAA	2460
QY	2461	GCCCTCAAGAGCTTGAAGAC CAGGCAAGTGA CATTATAGGCCATGGGCTTAA CCCCCTGAGCT	2520
Db	2461	GCCCTCAAGAGCTTGAAGAC CAGGCAAGTGA CATTATAGGCCATGGGCTTAA CCCCCTGAGCT	2520
QY	2521	TGCA CACAGGAGCCTCAAGTGA CCTCCAGGGGAC CACTG CAGA CAGGTGGCCTTTATCC	2580
Db	2521	TGCA CACAGGAGCCTCAAGTGA CCTCCAGGGGAC CACTG CAGA CAGGTGGCCTTTATCC	2580
QY	2581	CCAAAGAGCAACCA TTTGGCA TAGTGGCTGCAANTGGGAATGCAAGTTCAGTCAAGTCC	2640
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Qy 2701 CCAACCCACATAAGGGAGTGAATCTATCTAGGGGGCTGGCGACTTTGGGAGACACAC 2760
Db 2701 CCAACCCACATAAGGGAGTGAATCTATCTAGGGGGCTGGCGACTTTGGGAGACACAC 2760
Qy 2761 ATTAATGAGAGTGTGAG 2820
Db 2761 ATTAATGAGAGTGTGAG 2820
Qy 2821 TCTAGAGCTATATTTGAGAGGTGACAGTATAGAGTGGAGAGAGAGAGAGAGAGAGT 2880
Db 2821 TCTAGAGCTATATTTGAGAGGTGACAGTATAGAGTGGAGAGAGAGAGAGAGAGAGT 2880
Qy 2881 TCTGAGGTGTGAGAGGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 2940
Db 2881 TCTGAGGTGTGAGAGGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 2940
Qy 2941 CACAAATGTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3000
Db 2941 CACAAATGTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3000
Qy 3001 TGAAGAGACAGT 3060
Db 3001 TGAAGAGACAGT 3060
Qy 3061 CCAAGT 3120
Db 3061 CCAAGT 3120
Qy 3121 GGAAGT 3180
Db 3121 GGAAGT 3180
Qy 3181 TAAATCTCTGGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3240
Db 3181 TAAATCTCTGGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3240
Qy 3241 GGGGAGT 3300
Db 3241 GGGGAGT 3300
Qy 3301 CTGGGAGT 3360
Db 3301 CTGGGAGT 3360
Qy 3361 CCTATCATGTCCAAACATCATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3420
Db 3361 CCTATCATGTCCAAACATCATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3420
Qy 3421 GAAATCTGAGT 3480
Db 3421 GAAATCTGAGT 3480
Qy 3481 ACTGAGT 3540
Db 3481 ACTGAGT 3540
Qy 3541 GGTGTGTGTAAATTTGGCCAAAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGT 3600
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Qy 3601 TGTATGATGAGCTGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3660
Db 3601 TGTATGATGAGCTGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3660
Qy 3661 CTAAGCTTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3720
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Db 3721 TACAGACAGTATCTGTATACAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGT 3780
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Db 3781 TCAAGT 3840
Qy 3841 TGTCTCTGGGAGT 3900
Db 3841 TGTCTCTGGGAGT 3900
Qy 3901 GCTGAGT 3960
Db 3901 GCTGAGT 3960
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Db 3961 TGTGTGTGTGAGT 4020
Qy 4021 TTGTTCAACTCAACCTTTCAGATTAATAATAATAATAATAATAATAATAATAATA 4080
Db 4021 TTGTTCAACTCAACCTTTCAGATTAATAATAATAATAATAATAATAATAATAATA 4080
Qy 4081 GTGTGAGT 4140
Db 4081 GTGTGAGT 4140
Qy 4141 GGGGAGT 4200
Db 4141 GGGGAGT 4200
Qy 4201 GCAAGT 4260
Db 4201 GCAAGT 4260
Qy 4261 TTCTAAGT 4320
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Qy 4321 AAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 4380
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Qy 4381 CCTATCATGTCCAAACATCATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGT 4440
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Db 4441 AAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 4500
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Db 4501 CCACTCCATATCATGTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 4560
Qy 4561 AGT 4620
Db 4561 AGT 4620
Qy 4621 TATGAGATGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 4680
Db 4621 TATGAGATGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 4680
Qy 4681 GGTGAAGT 4740
Db 4681 GGTGAAGT 4740
Qy 4741 GGAAGT 4800
Db 4741 GGAAGT 4800
Qy 4801 GGAAGT 4860
Db 4801 GGAAGT 4860
Qy 4861 GGAAGT 4920
Db 4861 GGAAGT 4920
Qy 4921 GGAAGT 4980
Db 4921 GGAAGT 4980
Qy 4981 GGAAGT 5040
Db 4981 GGAAGT 5040

QY 4801 CCACGAGCTGGGAAGTTCTCAGTGGCAGGAGGTTTCCACAAGAAAACATGATGCCCT 4860
 DB 4509 CCACGAGCTGGGAAGTTCTCAGTGGCAGGAGGTTTCCACAAGAAAACATGATGCCCT 4568
 QY 4861 TCCCTTAAGCTGATCTTCCATCTTCTCCCTGGGAGTCTCTCCCGTCTTGGTTATC 4920
 DB 4569 TCCCTTAAGCTGATCTTCCATCTTCTCCCTGGGAGTCTCTCCCGTCTTGGTTATC 4628
 QY 4921 TGGGCTTGTGTTCAAGCAAGATTGGCTGCTGCTGCTCACTCACTCTTCTCTACTG 4980
 DB 4629 TGGGCTTGTGTTCAAGCAAGATTGGCTGCTGCTGCTCACTCACTCTTCTCTACTG 4688
 QY 4981 CTCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 5040
 DB 4689 CTCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 4748
 QY 5041 TTTTCTCCCTTCTCAATTGATTCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5100
 DB 4749 TTTTCTCCCTTCTCAATTGATTCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4808
 QY 5101 CTTCCTTCT 5160
 DB 4809 CTTCCTTCT 4868
 QY 5161 CTGCTGAGAGTGTGAGATCAACCTGGGGTTCACACCTTATGTAACAATCTTCCA 5220
 DB 4869 CTGCTGAGAGTGTGAGATCAACCTGGGGTTCACACCTTATGTAACAATCTTCCA 4928
 QY 5221 GTGAGCACAAGCTTCAAGTGTGCTGCTCTTCACTTCTCTCAACCCCTGGTGTGTC 5280
 DB 4929 GTGAGCACAAGCTTCAAGTGTGCTGCTCTTCACTTCTCTCAACCCCTGGTGTGTC 4988
 QY 5281 CTGCTCATCTGTGTGAGATCTTGTAGATTGTCTCCAGCTCTGTACTCTCTTCTCT 5340
 DB 4989 CTGCTCATCTGTGTGAGATCTTGTAGATTGTCTCCAGCTCTGTACTCTCTTCTCTCT 5048
 QY 5341 GCGCTTCT 5400
 DB 5049 GCGCTTCT 5108
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 DB 5109 ATTCTTCAAGATTTCTGAAAAGTTAACAGAGTGAAGATTTTCCCTGTAGACAGACA 5168
 QY 5461 TCAGATTTCTCCGGAAGTCAAGCTTCCAGCTCTCTTCTCTCTGCCCAGCTGCCGCA 5520
 DB 5169 TCAGATTTCTCCGGAAGTCAAGCTTCCAGCTCTCTTCTCTCTGCCCAGCTGCCGCA 5228
 QY 5521 CTCCTTGAACAACCTCAAGGACCTTACCCCAATAGACCTCTGACAGAGAAGAGGACT 5580
 DB 5229 CTCCTTGAACAACCTCAAGGACCTTACCCCAATAGACCTCTGACAGAGAAGAGGACT 5288
 QY 5581 TTACATGAGTCTGTGTGAGAGCAATAGCTAGCTGTAAAAGAGCAGGAATGTGT 5640
 DB 5289 TTACATGAGTCTGTGTGAGAGCAATAGCTAGCTGTAAAAGAGCAGGAATGTGT 5348
 QY 5641 GGTGTGAAAAGTCAAGACTTTCATATGAAGCTTACCCACACCAAGATGACAGACA 5700
 DB 5349 GGTGTGAAAAGTCAAGACTTTCATATGAAGCTTACCCACACCAAGATGACAGACA 5408
 QY 5701 TCCCTCTATCTCCCAATAGAGTTGAGTCGAC 5735
 DB 5409 TCCCTCTATCTCCCAATAGAGTTGAGTCGAC 5443

RESULT 3

US-10-332-966-2

; Sequence 2, Application US/10332966

; Publication No. US20030188324A1

; GENERAL INFORMATION:

; APPLICANT: HASEGAWA, Koji

; APPLICANT: KAWASE, Yosuke

; APPLICANT: SUZUKI, Hiroshi
 ; TITLE OF INVENTION: p300 TRANSGENIC ANIMAL
 ; FILE REFERENCE: 382,1040
 ; CURRENT APPLICATION NUMBER: US/10/332,966
 ; CURRENT FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: PCT/JP01/06086
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: JP2000-215143
 ; PRIOR FILING DATE: 2000-07-14
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 5443
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: promoter
 ; LOCATION: (1)..(5443)
 US-10-332-966-2

Query Match 88.0%; Score 5045; DB 16; Length 5443;
 Best Local Similarity 93.9%; Pred. No. 0;
 Matches 5383; Conservative 0; Mismatches 60; Indels 292; Gaps 1;

QY 1 GGATCCTGCAAGTACACAAAGGATCTCCACACAGGAGCTTGTCAATTTCAGT 60
 DB 1 GGATCCTGCAAGTACACAAAGGATCTCCACACAGGAGCTTGTCAATTTCAGT 60
 QY 61 TTCATGCTTGTCTCACAATGTGAGCTTCCAGAGCTTAATTGACTTTGTTTAT 120
 DB 61 TTCATGCTTGTCTCACAATGTGAGCTTCCAGAGCTTAATTGACTTTGTTTAT 120
 QY 121 TTCAAAAGGCTGATGAGAGTATGTTGTGCTACCCAGCTCTAAGAGGAGCCGTA 180
 DB 121 TTCAAAAGGCTGATGAGAGTATGTTGTGCTACCCAGCTCTAAGAGGAGCCGTA 180
 QY 181 AGCCCTCAGACCTTGAGAGCTTGTGCAACAGCCCTTAAAGTGAAGAGAAATTAAGCAATT 240
 DB 181 AGCCCTCAGACCTTGAGAGCTTGTGCAACAGCCCTTAAAGTGAAGAGAAATTAAGCAATT 240
 QY 241 TCCTTAAAGCAAAATCTGCTGTAGACTTCTTCTCTGACCTTGAGCTTCTGAGGCTCT 300
 DB 241 TCCTTAAAGCAAAATCTGCTGTAGACTTCTTCTCTGACCTTGAGCTTCTGAGGCTCT 300
 QY 301 AGGATGGGAGAGTGGGCTTGAAGAAAGAGTGGGAAAGTGGCAAAAGCCGATCCCTTAG 360
 DB 301 AGGATGGGAGAGTGGGCTTGAAGAAAGAGTGGGAAAGTGGCAAAAGCCGATCCCTTAG 360
 QY 361 GGCCTGTGAAGTGTGAGAGCTTCCCTGTGACAGACTGCTCATAGATCTCTCCAGCC 420
 DB 361 GGCCTGTGAAGTGTGAGAGCTTCCCTGTGACAGACTGCTCATAGATCTCTCCAGCC 420
 QY 421 AAACATAGCAAGATGATACCTCTTGTGACTTCCAGAGCCAGTACCTGTGAGTT 480
 DB 421 AAACATAGCAAGATGATACCTCTTGTGACTTCCAGAGCCAGTACCTGTGAGTT 480
 QY 481 GAAAAGAGTTTAAAGAAAGCTTGTGAACCTGTAACCTGTAAGTCTATCCACCAAGA 540
 DB 481 GAAAAGAGTTTAAAGAAAGCTTGTGAACCTGTAACCTGTAAGTCTATCCACCAAGA 540
 QY 541 AGCAGCTAGTGCACCTGTAGTTAGTACCTAGCTGATTAATATGACAGAGTGGCCAC 600
 DB 541 AGCAGCTAGTGCACCTGTAGTTAGTACCTAGCTGATTAATATGACAGAGTGGCCAC 600
 QY 601 AGAAGTCTGTGGGTGAGAACTGACCAAGTACTTTTCAAGTGGCAAGATGACCCCC 660
 DB 601 AGAAGTCTGTGGGTGAGAACTGACCAAGTACTTTTCAAGTGGCAAGATGACCCCC 660
 QY 661 TCAGCAGATGTAGTATGTCCTCTTGAATCCATCCCAAGCAGAGTCTTCAAGAGACATG 720
 DB 661 TCAGCAGATGTAGTATGTCCTCTTGAATCCATCCCAAGCAGAGTCTTCAAGAGACATG 720
 QY 721 GGATGAGATGTAGTATGTCATTCGAAACAGAGTATCCAGAGTCCCTTGCCTCC 780

D	b		4809	CTTCCTTCCCTCCTTTCTCCCTCCCTTCCTTCCTTCCTTCCTTCCTTCCTTC	4868
O	y		5161	CTGTGTCAGAGTGCTGAGAATCACACCTGGGGTTCCAACCTTAATGTAACAATCTTCCA	5220
D	b		4869	CTGTGTCAGAGTGCTGAGAATCACACCTGGGGTTCCCAACCCTTAATGTAACAATCTTCCA	4928
O	y		5221	GTCAGGCCACAGATTAGTGCTGTGGGTGCTCTTAACTTCCTCGAACCCCCGGCTGTGC	5280
D	b		4929	GTGAACCCACAGCTTCAGTGCTGTGGGTGCTCTTAACTTCCTCGAACCCCCGGCTGTGC	4988
O	y		5281	CTGTTCACCTGTGTGTCAGAGATCTAGATTGGTGTCCAGACTCTGTACTCTCTTCCT	5340
D	b		4989	CTGTTCACCTGTGTGTCAGAGATCTAGATTGGTGTCCAGACTCTGTACTCTCTTCCT	5048
O	y		5341	GCCTGTTCTCTCTGTGTCCAGCTGGCACACTGTGGTGCTGTTCAGCTGTGGTCCAC	5400
D	b		5049	GCCTGTTCTCTCTGTGTCCAGCTGGCACACTGTGGTGCTGTTCAGCTGTGGTCCAC	5108
O	y		5401	ATTCTTCAGAGTTCCTGTAAAAATTAACTCAGGTGAGAAATGTTTTCCCTGTAGACAGCAGA	5460
D	b		5109	ATTCTTCAGAGTTCCTGTAAAAATTAACTCAGGTGAGAAATGTTTTCCCTGTAGACAGCAGA	5168
O	y		5461	TTCAGATTCTCCCGGAAGTTCAGAGCTTCCAGCCCTCTTTCTCTGCCAGCTGCCCGCA	5520
D	b		5169	TTCAGATTCTCCCGGAAGTTCAGAGCTTCCAGCCCTCTTTCTCTGCCAGCTGCCCGCA	5228
O	y		5521	CTCTTAGCAAACTTCAGGCACCTTACCACATAGACTCTGACAGAGAACAGCAGACT	5580
D	b		5229	CTCTTAGCAAACTTCAGGCACCTTACCACATAGACTCTGACAGAGAACAGCAGACT	5288
O	y		5581	TTAATCATGAGTCTCTGTGGAGAGCCATTAGGCTAAGGTATAAAGAGCGAGGAATGGT	5640
D	b		5289	TTAATCATGAGTCTCTGTGGAGAGCCATTAGGCTAAGGTATAAAGAGCGAGGAATGGT	5348
O	y		5641	GGTGTAGAAAAGTTCAGGACTTCACATAGAAAGCTTAGCCACACCGAATAATGACAGACAGA	5700
D	b		5349	GGTGTAGAAAAGTTCAGGACTTCACATAGAAAGCTTAGCCACACCGAATAATGACAGACAGA	5408
O	y		5701	TCCCTTCCTATCTCCCCCATTAAGATTGATGTGAC	5735
D	b		5409	TCCCTTCCTATCTCCCCCATTAAGATTGATGTGAC	5443

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RESULT 4
US-10-944-375-15
; Sequence 15, Application US/10944375
; Publication No. US20050066381A1
; GENERAL INFORMATION:
; APPLICANT: Cincinnati Children's Hospital Medical Center
; APPLICANT: University of Cincinnati
; APPLICANT: Molkenstin, Jeffery D
; APPLICANT: Kraniak, Evangelia G
; TITLE OF INVENTION: REGULATION OF CARDIAC CONTRACTILITY AND HEART FAILURE PROPENSITY
; FILE REFERENCE: 9761M#L
; CURRENT APPLICATION NUMBER: US/10/944,375
; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: US 60/503,853
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 5443
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-944-375-15

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Query Match	88.0%	Score 5045	DB 21	Length 5443
Best Local Similarity	93.9%	Pred. No. 0		
Matches 5383	Conservative 0	Mismatches 60	Indels 292	Gaps 1
QY	1	GGATCTGCAAGGTACACAAAGGCTCCACCACCAAGTGGCCCTAGTCTCAATTTCGT	60	

D	b	1	GGATCTCGCAAGGTCACACAAGGGTCTCCACCCACACAGGTGGCCCTAGTCTCAATTCCAGT	60
O	y	61	TTCCATCCCTTGTTCTGCACATGCTGGCTCTCCCGACAGCTAAATTGGACTTTGTTTTAT	120
D	b	61	TTCCATCCCTTGTTCTGCACATGCTGGCTCTCCCGACAGCTAAATTGGACTTTGTTTTAT	120
O	y	121	TTCAAAAGGGCCCTGAAATGAGAGATGATCTTTGATGCTAACCGCTTAAAGGGTCCCGTGA	180
D	b	121	TTCAAAAGGGCCCTGAAATGAGAGATGATCTTTGATGCTAACCGCTTAAAGGGTCCCGTGA	180
O	y	181	AGCCCTCAGACTGGAGCTCTTGGCAACAGCCCTTTAGGTGGAAGCAGAAATTAAGCAATTT	240
D	b	181	AGCCCTCAGACTGGAGCTCTTGGCAACAGCCCTTTAGGTGGAAGCAGAAATTAAGCAATTT	240
O	y	241	TCCTTAAAGCCAAATATCTGCTCTAGACTCTTCTTCTGACCTCGGTCTCTGGGCTCT	300
D	b	241	TCCTTAAAGCCAAATATCTGCTCTAGACTCTTCTTCTGACCTCGGTCTCTGGGCTCT	300
O	y	301	AGGGTGGGGAGGTGGGGCTTGGAAAGAAAGTGGGGAAATGGCAAAAGCCGATCCCTAG	360
D	b	301	AGGGTGGGGAGGTGGGGCTTGGAAAGAAAGTGGGGAAATGGCAAAAGCCGATCCCTAG	360
O	y	361	GGCCCTGTGAAGTTGGAGCCCTTCCGTACAGACTGGCTCATAGATTCCTCCCTCAGCC	420
D	b	361	GGCCCTGTGAAGTTGGAGCCCTTCCGTACAGACTGGCTCATAGATTCCTCCCTCAGCC	420
O	y	421	AAACATAGCAAGAAAGTATACCTCTTTGTGACTTCCCAAGGCCAGTACCTGTCAAGTT	480
D	b	421	AAACATAGCAAGAAAGTATACCTCTTTGTGACTTCCCAAGGCCAGTACCTGTCAAGTT	480
O	y	481	GAAACAGATTTAGAGAAAGCTCTGAACTCACTGAACTGTGAAGCTCATTCACACAAACA	540
D	b	481	GAAACAGATTTAGAGAAAGCTCTGAACTCACTGAACTGTGAAGCTCATTCACACAAACA	540
O	y	541	AGCACTAGGCGCACATGCTAGTTAGATATCTCAGCTAGATAAATATGACAGAGCTGGGCGAC	600
D	b	541	AGCACTAGGCGCACATGCTAGTTAGATATCTCAGCTAGATAAATATGACAGAGCTGGGCGAC	600
O	y	541	AGCACTAGGCGCACATGCTAGTTAGATATCTCAGCTAGATAAATATGACAGAGCTGGGCGAC	600
D	b	601	AGAGTCCCTGGGGTGTAGGAATGACCAAGTACTTTTCAGTGGCAAAAGGTATGACCCCC	660
O	y	601	AGAGTCCCTGGGGTGTAGGAATGACCAAGTACTTTTCAGTGGCAAAAGGTATGACCCCC	660
D	b	601	AGAGTCCCTGGGGTGTAGGAATGACCAAGTACTTTTCAGTGGCAAAAGGTATGACCCCC	660
O	y	661	TCAGCAGATGTAGTAATGTCCCTTAAATGCCATCCCAAGGAGGTCTCTTAAGAGAAATG	720
D	b	661	TCAGCAGATGTAGTAATGTCCCTTAAATGCCATCCCAAGGAGGTCTCTTAAGAGAAATG	720
O	y	721	GGATGAGAGATGTATGATATGATGGCAATTCAAACACAGTATCCACAGATGTCCTTGGCCC	780
D	b	721	GGATGAGAGATGTATGATATGATGGCAATTCAAACACAGTATCCACAGATGTCCTTGGCCC	780
O	y	781	TTCCACTTAGCCAGAGAGACAGTAACCTTAGCTATCTTTCTTCCCTCCCATCTCTCCAG	840
D	b	781	TTCCACTTAGCCAGAGAGACAGTAACCTTAGCTATCTTTCTTCCCTCCCATCTCTCCAG	840
O	y	841	GACACACCCCTGCTGCTGACAGTATTCATTTCTTCTTCAAGTCCCTCTGTGACTTCCAT	900
D	b	841	GACACACCCCTGCTGCTGACAGTATTCATTTCTTCTTCAAGTCCCTCTGTGACTTCCAT	900
O	y	901	TTTGCAAGGCTTTTAACTCTGACCTGTGGAAATATGAGTGTGGCCCTGAGGTGGGCAA	960
D	b	901	TTTGCAAGGCTTTTAACTCTGACCTGTGGAAATATGAGTGTGGCCCTGAGGTGGGCAA	960
O	y	961	GCCATCTCAAGAGAAAGCAGACAACAGGGGAGCCAGATTTTGGAGAGATCAGAACTTAA	1020
D	b	961	GCCATCTCAAGAGAAAGCAGACAACAGGGGAGCCAGATTTTGGAGAGATCAGAACTTAA	1020
O	y	1021	TCACCTGGGGGCTGGGGGTGAAAAAAGATGATGATGAGTCCGCTCCAGCTAAACCAAGC	1080
D	b	1021	TCACCTGGGGGCTGGGGGTGAAAAAAGATGATGATGAGTCCGCTCCAGCTAAACCAAGC	1080
O	y	1081	TAGTCTCCCGAATATCTCTGCAACAGCTGGGCTGCTCGGGGTAGCTTTAAGAAATGTGGGTC	1140
D	b	1081	TAGTCTCCCGAATATCTCTGCAACAGCTGGGCTGCTCGGGGTAGCTTTAAGAAATGTGGGTC	1140

QY 1141 TGAAGCAATGGGATTGGAAGCATCTCTTGAAGTCTCCCTCAACCCCACTAGAGAC 1200
Db 1141 TGAAGCAATGGGATTGGAAGCATCTCTTGAAGTCTCCCTCAACCCCACTAGAGAC 1200
QY 1201 ACACTGCTGTGTGGCAGACTCCTGTTCACACAGCCCTGTGTGTGACCACTGAGCTAG 1260
Db 1201 ACACTGCTGTGTGGCAGACTCCTGTTCACACAGCCCTGTGTGTGACCACTGAGCTAG 1260
QY 1261 GCAACCAAGCATGGGCTCTGTCTGAGATGGAAGTTGGTTACCAATGCAAAAACAG 1320
Db 1261 GCAACCAAGCATGGGCTCTGTCTGAGATGGAAGTTGGTTACCAATGCAAAAACAG 1320
QY 1321 CAGGGAGGGGAGACAGAGAAATTAAGGAAGAAAGGAAAGGCAAGTCAATCAG 1380
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QY 1441 AGATTCTGGGCAATAGGAGGCCACAGAAAGAGGCCAGGCCCAAGTCTCTCTTT 1500
Db 1441 AGATTCTGGGCAATAGGAGGCCACAGAAAGAGGCCAGGCCCAAGTCTCTCTTT 1500
QY 1501 ATACCCCTCATCCGCTCCCAATTAAAGCCCACTCTTCTCTGATCAGACCTGAGCTGC 1560
Db 1501 ATACCCCTCATCCGCTCCCAATTAAAGCCCACTCTTCTCTGATCAGACCTGAGCTGC 1560
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Db 1621 GCAACTTAAGAGCCAGACCTAAAGAGAGAGATTAAGGTCTTCAAAAGTGGCCAG 1680
QY 1681 CTGTGCAACAGAGGCTGAGAGCTGTGTGTAGAGCTCAAGATTAAGATGATGCTCAG 1740
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Db 1741 ATGGGCGGGGGGGGATTTCTGGGGGGGGGAGAGAGAGTGAAGAGACCTGGAACAG 1800
QY 1801 AGAATCTGGAAGGCTGGAACGATTAACATTAAGGGAAGAACCCAGGCTTCTTTAGATG 1860
Db 1801 AGAATCTGGAAGGCTGGAACGATTAACATTAAGGGAAGAACCCAGGCTTCTTTAGATG 1860
QY 1861 TAAATCATGAAACAGAGGAGAGAGAGAGTGAAGAGATGGAAGAGACCCCGGGGCAAG 1920
Db 1861 TAAATCATGAAACAGAGGAGAGAGAGAGTGAAGAGATGGAAGAGACCCCGGGGCAAG 1920
QY 1921 CATGAAGCAAGGAGACCAAGGTTGAGCGCTCCGTGAATCAGCCTGTGAGAGCAGAG 1980
Db 1921 CATGAAGCAAGGAGACCAAGGTTGAGCGCTCCGTGAATCAGCCTGTGAGAGCAGAG 1980
QY 1981 CCCTGTATGAGACCAAGCAAGAGGCTAGAGGTTAATGTGAGACAGGGAACAGAG 2040
Db 1981 CCCTGTATGAGACCAAGCAAGAGGCTAGAGGTTAATGTGAGACAGGGAACAGAG 2040
QY 2041 GTGAGACAGGGAACAGACAGAGAGCGGGGAGCCAGGTTAACAAAGGAATGTTCTTCAC 2100
Db 2041 GTGAGACAGGGAACAGACAGAGAGCGGGGAGCCAGGTTAACAAAGGAATGTTCTTCAC 2100
QY 2101 CTGTGGCAGAGGCTCATCTGTGTCCACTACTTGAATGTTCACTGACAGCTGCAAGGC 2160
Db 2101 CTGTGGCAGAGGCTCATCTGTGTCCACTACTTGAATGTTCACTGACAGCTGCAAGGC 2160
QY 2161 TGGCTTGGAGGCACTGGAAGAGTATGTAAGAGCCAGGGGAGACAAAGGGGCTTAGGA 2220
Db 2161 TGGCTTGGAGGCACTGGAAGAGTATGTAAGAGCCAGGGGAGACAAAGGGGCTTAGGA 2220

QY 2221 AAGGAAGAGAGGCAAAACAGGCCACACAGAGGGCAGAGGCCAGAACTGATTAATCT 2280
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QY 2281 CTTCCTGTGTGATCTTCATAGAGAGAGTGGGAACTGTGACCAACCATCCCATGA 2340
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QY 2341 GCGCCCACTAACCAATACCAAGTTGGGCTGAGTGGATCTAGTGTCCCTGAGGAGAG 2400
Db 2341 GCGCCCACTAACCAATACCAAGTTGGGCTGAGTGGATCTAGTGTCCCTGAGGAGAG 2400
QY 2401 CCTGGCTTGTCTCTGAGACCTGACCCAGGCTGACCCCAATGTTCTCAGTACTTGAAT 2460
Db 2401 CCTGGCTTGTCTCTGAGACCTGAGCCTGAGCCAGCTGACCCCAATGTTCTCAGTACTTGAAT 2460
QY 2461 GCGCTCAAGAGCTTGAAGCAAGGAGTGAATTTAGGCAATGGGCTAACCCTGAGCT 2520
Db 2461 GCGCTCAAGAGCTTGAAGCAAGGAGTGAATTTAGGCAATGGGCTAACCCTGAGCT 2520
QY 2521 TGCACACAGAGGCTCAAGTGAACCTTCAGGAGACAGCTGACAGAGGTTGATCC 2580
Db 2521 TGCACACAGAGGCTCAAGTGAACCTTCAGGAGACAGCTGACAGAGGTTGATCC 2580
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Db 2581 CCAAGAGCAACCATTTGAGATAGGTGCTGCAAAATGGAATGCAAGTTGAATCAGTTC 2640
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Db 2641 CCTTCAGAAATCTGATGCAAGACCTTAAGACCTCTGAGAGAGGGTATGCTCTGCC 2700
QY 2701 CCAACCACTAAGGGGAGTGAATCTTCTAGGGGCTGGCCACCTTGGGAGACACAC 2760
Db 2701 CCAACCACTAAGGGGAGTGAATCTTCTAGGGGCTGGCCACCTTGGGAGACACAC 2760
QY 2761 ATTAAGAGAGTGTGAGGCCAGAAAACAGACCCGCTGTGTCTGACCACCTCCACAC 2820
Db 2761 ATTAAGAGAGTGTGAGGCCAGAAAACAGACCCGCTGTGTCTGACCACCTCCACAC 2820
QY 2821 TCTAGAGCTAATTTAGAGAGTGAACATAGATAGGGTGGAGCTGTGAGCAGGAGAGTGT 2880
Db 2821 TCTAGAGCTAATTTAGAGAGTGAACATAGATAGGGTGGAGCTGTGAGCAGGAGAGTGT 2880
QY 2881 TCTGTGTGTGAGGCTGTGAGGGAAGACAGACAGGAGAGTGTGCTTGTCTCTGAA 2940
Db 2881 TCTGTGTGTGAGGCTGTGAGGGAAGACAGACAGGAGAGTGTGCTTGTCTCTGAA 2940
QY 2941 CACAATGTCTACTAGTTAATACAGCATGACCTGTGAAGACCCCAATCTACGACCTC 3000
Db 2941 CACAATGTCTACTAGTTAATACAGCATGACCTGTGAAGACCCCAATCTACGACCTC 3000
QY 3001 TGAAGAGCAGCAGCCCTGAGAGACAGGGGTTGTCTTGAAGCTTGGGCTTGTGATGTG 3060
Db 3001 TGAAGAGCAGCAGCAGCCCTGAGAGACAGGGGTTGTCTTGAAGCTTGGGCTTGTGATGTG 3060
QY 3061 CCACAAGAGAGGCTAGATGTGATTAAGGCCCAAGAGGTTTGAAGAGGCACTTG 3120
Db 3061 CCACAAGAGAGGCTAGATGTGATTAAGGCCCAAGAGGTTTGAAGAGGCACTTG 3120
QY 3121 GGAAGGGGTCAGTCTGACAGAGCCCTATCATGGAATCTGAGGCTGGGGCCAACTGTGTG 3180
Db 3121 GGAAGGGGTCAGTCTGACAGAGCCCTATCATGGAATCTGAGGCTGGGGCCAACTGTGTG 3180
QY 3181 TAAATCTGTGGCTGTGCAAGGATTAAGAGCACTTGCAATCTTGTGCAAGCTTGAGG 3240
Db 3181 TAAATCTGTGGCTGTGCAAGGATTAAGAGCACTTGCAATCTTGTGCAAGCTTGAGG 3240
QY 3241 GCGGGAAGGAGCAACCCCTCACTTATACCTTTTCTCCTCAGGCCCAAGATTAACACT 3300
Db 3241 GCGGGAAGGAGCAACCCCTCACTTATACCTTTTCTCCTCAGGCCCAAGATTAACACT 3300
QY 3301 CTGGCTTCCCTCCACTCCCATCAAGATGAGGAGGTTGACAGAGGAGGTTAAAAA 3360

|||||
Db 3301 CTGGCCCTCCCTCCCTCCATCCAGAGGAGGCTTCAGAGGAGGATAAAA 3360
OY 3361 CCTACATGTCACCAACATCATGTCAGATATATGATCTCATGTCATAGAGCAAGAAA 3420
Db 3361 CCTACATGTCACCAACATCATGTCAGATATATGATCTCATGTCATAGAGCAAGAAA 3420
OY 3421 GGAATCTGAGAGCTTAATCTGGTTAATGTTAAAGTCTGTGTGATGTGTGTCTG 3480
Db 3421 GGAATCTGAGAGCTTAATCTGGTTAATGTTAAAGTCTGTGTGATGTGTGTCTG 3480
OY 3481 ACTGAAAACGGGATGAGCTGTGACAGTCTGATCTGTGTGTGAGGTTACAGACTGCA 3540
Db 3481 ACTGAAAACGGGATGAGCTGTGACAGTCTGATCTGTGTGTGAGGTTACAGACTGCA 3540
OY 3541 GGTGTGTGTAAATTCGCCAAGGCAAAAGTGGGTAATCCCTTCATGATTTAAAGAT 3600
Db 3541 GGTGTGTGTAAATTCGCCAAGGCAAAAGTGGGTAATCCCTTCATGATTTAAAGAT 3600
OY 3601 TGAATGATGAGCTGATCTCAAGGACCATGAAAATGAAATGACACTATATGTCT 3660
Db 3601 TGAATGATGAGCTGATCTCAAGGACCATGAAAATGAAATGACACTATATGTCT 3660
OY 3661 CTAAAGCTTAAGTACCAAGTCTTTGAGAGACCTGTCTAGAGATGTTGGCAACAGAC 3720
Db 3661 CTAAAGCTTAAGTACCAAGTCTTTGAGAGACCTGTCTAGAGATGTTGGCAACAGAC 3720
OY 3721 TACAGACATATCTGTACAGATTAAGAGAGAGAGAGGAGGTTAGAAATTTCTTACTA 3780
Db 3721 TACAGACATATCTGTACAGATTAAGAGAGAGAGAGGAGGTTAGAAATTTCTTACTA 3780
OY 3781 TCAAAAGGAAAATGAGTGTGACACTTGCAAAAGTGAATGCTCTCCCTAGACATGACTT 3840
Db 3781 TCAAAAGGAAAATGAGTGTGACACTTGCAAAAGTGAATGCTCTCCCTAGACATGACTT 3840
OY 3841 TGTCTCTGGGAGGACAGACACTGTGAACTTCAAGTCTGAGAGATGAGAGCTCCCTCA 3900
Db 3841 TGTCTCTGGGAGGACAGACACTGTGAACTTCAAGTCTGAGAGATGAGAGCTCCCTCA 3900
OY 3901 GCTGGAAGCTATGAGATTAAGCAAGGTTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 3960
Db 3901 GCTGGAAGCTATGAGATTAAGCAAGGTTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 3960
OY 3961 TGTGTGTGAGAGGACAGAGGACAGATTAAGCTTGAAGAGAGGATCCCTTACCAG 4020
Db 3961 TGTGTGTGAGAGGACAGAGGACAGATTAAGCTTGAAGAGAGGATCCCTTACCAG 4020
OY 4021 TTTGTTCAACTCACTCTTCAATTAATACTGAAGTGAAGGAGGAGGAGGAGGAGGAGG 4080
Db 4021 TTTGTTCAACTCACTCTTCAATTAATACTGAAGTGAAGGAGGAGGAGGAGGAGGAGG 4080
OY 4081 GTGTGAGACGCTCTGTCTCTCTCTGATGACCTTGAAGGAGGAGGAGGAGGAGGAGG 4140
Db 4081 GTGTGAGACGCTCTGTCTCTCTCTGATGACCTTGAAGGAGGAGGAGGAGGAGGAGG 4140
OY 4141 GCTTGAAGCTCTCTGTCTCTCTCTGATGACCTTGAAGGAGGAGGAGGAGGAGGAGG 4200
Db 4141 GCTTGAAGCTCTCTGTCTCTCTCTGATGACCTTGAAGGAGGAGGAGGAGGAGGAGG 4200
OY 4201 GCAAACTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4260
Db 4201 GCAAACTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4260
OY 4261 TTCTTAAAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4320
Db 4261 GGAACCCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4320
OY 4321 AAGTGAAGTTTACCACTTCTATCAATGATGAGAGAGGAGGAGGAGGAGGAGGAGG 4380
Db 4321 AAGTGAAGTTTACCACTTCTATCAATGATGAGAGAGGAGGAGGAGGAGGAGGAGG 4380
OY 4381 CCTATCACTGATAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4440
Db 4381 CCTATCACTGATAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4440

----- 4291
OY 4441 AAGTGAAGTTTACCACTTCTATCAATGATGAGAGAGGAGGAGGAGGAGGAGGAGG 4500
Db 4292 ----- 4291
OY 4501 CCACTTCTATCACTGATAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4560
Db 4292 ----- 4291
OY 4561 AGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620
Db 4292 ----- 4291
OY 4621 TATGAGATGAGATATATAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4680
Db 4329 TATGAGATGAGATATATAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4388
OY 4681 GGTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4740
Db 4389 GGTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4448
OY 4741 GGAAGCTGCTTCTGGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4800
Db 4449 GGAAGCTGCTTCTGGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4508
OY 4801 CCAACAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4860
Db 4509 CCAACAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4568
OY 4861 TCCCTTAAGCTGATCTTCTCATTTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4920
Db 4569 TCCCTTAAGCTGATCTTCTCATTTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4628
OY 4921 TTGGCTCTTGTGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4980
Db 4629 TTGGCTCTTGTGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4688
OY 4981 CTCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 5040
Db 4689 CTCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 4748
OY 5041 TTTTCTCCCTTCTCATTTGATTAATTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5100
Db 4749 TTTTCTCCCTTCTCATTTGATTAATTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4808
OY 5101 CTTCCTTCT 5160
Db 4809 CTTCCTTCT 4868
OY 5161 CTGTGTCAAGTGTGAGATCAACACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5220
Db 4869 CTGTGTCAAGTGTGAGATCAACACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4928
OY 5221 GTGAGCAACAGCTTCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5280
Db 4929 GTGAGCAACAGCTTCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4988
OY 5281 CTGTTCATCTGTGATGAGATCTCTGATTTGATGATGATGATGATGATGATGATGATGATG 5340
Db 4989 CTGTTCATCTGTGATGAGATCTCTGATTTGATGATGATGATGATGATGATGATGATGATG 5048
OY 5341 GCTGTGTCT 5400
Db 5049 GCTGTGTCT 5108
OY 5401 ATTCTTCAAGATTTCTGAAAAGTTTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5460
Db 5109 ATTCTTCAAGATTTCTGAAAAGTTTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5168
OY 5461 TCAAGATTTCTCCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5520
Db 5169 TCAAGATTTCTCCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5228

Db	3530	CATCCATGTACACAAAAGAAAGTAAAGAAAAGAAATCTGCAGACTGGAGTGGTAAAGTGA	3589
QY	3453	AAAGTCTGTGTGCATGTGTGTGTGTCTGACCTGAAAACGGGCGATGCTGTGACGCTTTTCA	3512
Db	3590	AAAATCTGCATGTGTGTGCTGTAAGATGGGCACAGACACGGTCAAG-----	3633
QY	3513	GTTCGTGCGCGAAGGTTACAGACCTGCAGGTTTGTTGTATAATTGGCCCAAGCAAGTGG	3572
Db	3634	--TCTGTATGTGAAGTGTCTGAACCTGGGGTTCGTGTGTAATAATCTGCTTAGCGCGCAGG	3691
QY	3573	GTGAATCCCTTCCATGTGTTTAAAGAGATGGATGATGGCTGCATCTCAAGACCATGGA	3632
Db	3692	GAGAAATCACTGCCATTTGTGTGATGACGAGGTGGATGTGGCCACTCTATC-AAGAGCATTTAG	375E
QY	3633	AAATGAATGAGACACTCTATATGTGTCTCTAAGCTAAAGTAG--CAAGGCTTTTGAGG	3689
Db	3751	GGAAGGGGTGGGGACTCCAGACGTGTCCCAACCAAGGATGGCTTCAAGACTTGGGAGA	3810
QY	3690	ACACCTGTCTTGAAGATGTGGGCACACAGAGACTACAGACAGTATCTGTACAGATTAAGAG	3749
Db	3811	ACACTTGTCTGTAAACATTGGGGAAACG-----AAGGAAACAGGCAATGGCACTTAATGACG	3865
QY	3750	AGAGAGAGGGGGGTGTGAATTTCTTCTACTATCAAGGGGAAACGTAGTGTGACACTGCA	3809
Db	3866	ACTGAGGCCACGAGACAGAA-----TTTCTCTACAAAAGAAAATGAGCATGAGATGGA	3919
QY	3810	AAGTGATGTCTCTCCCTAGACATCATGACTTTGTCTCTGGGAGCCAGCACTGTGGAAT	3868
Db	3920	CAACAGATCCCTTCCCTGGGCA--CATACTGACGTTTATGTCCTTACCATTTGGGGCTC	3977
QY	3870	TCAGGTCTGAAGAGTGAAGAGCTTCCTCAAGCTGGAAGCTATGCATTAAGCCAGGTTTG	3929
Db	3978	CAGTACTAAACAGCAGGAAGATGCTCCAGCCTTGGGACTGTGTAGGGGATGTCAAGAAATGG	4037
QY	3930	AAAGG-GGGAAGGGAGAGCCTGGGATGGGAGCTTGTGTGTTGGAGCAGGGGACAGATAT	3988
Db	4038	AAAGGAAGGCTGGGGGAACAGGGGAGGAAGAACCCATGTGTTGAGGCGGAGGACAGGCAT	4097
QY	3989	TAACTCTGAAGAGAGAGGTGACCCCTTACCAGTTGTTCAACTCAACCTTTCAGATTAAAAA	4048
Db	4098	TTGGCCTGTCAAGAGAAGGTGACCTCTCACCCATGTTTTTC-AATCTCACTTCGGGGGAAAAA	4156
QY	4049	TAACTGAGTTAAGGCG-----CTGGGTATGGGAGGTGTGTGAGACGCTCTGTCTTCC	4103
Db	4157	TAACTGAGGTAAAGGCGCATGTGCAGGGTGTGGAGAGGCGGTGTAGAAAGGTCTGTCTTCC	4216
QY	4104	TC-TCGATGCGCCTGAGGCGCTTTTGGGAGGAGAG--AATGTGCCCAAGGACTTAAAAAAGG	4166
Db	4217	ACATATCTGCTCATCAAGCCCTTTTGAAGGGGAGTATGTGCCCTTAAAGGACTTAAAAAAGG	4276
QY	4161	CCATGAGGCCAGAGGGGCGAAGGGCAACAGACTTTTCATGTGGCAAACTTGGGGGCC	4216
Db	4277	CCGTGAGCCAGAGAAGGCTGGGGGACGACGACTTTCTTGGGCAAAATCAGGGGGGCC	4332
RESULT 7			
US-10-798-037-1			
; Sequence 1, Application US/10798037			
; Publication No. US20040229360A1			
; GENERAL INFORMATION:			
; APPLICANT: Robbins, Jeffrey			
; APPLICANT: Children's Hospital Medical Center			
; TITLE OF INVENTION: Cardiac-Preferred Genetic Alteration of			
; FILE REFERENCE: CHM02/GN054			
; CURRENT APPLICATION NUMBER: US/10/798,037			
; CURRENT FILING DATE: 2004-03-11			
; PRIOR APPLICATION NUMBER: 60/454,947			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 5190			

QY	DB	Query Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps
QY	2099	ACCTGTGGCCAGAGCCGTTCAT-CTGTGTCCACATACTCTTGAATGTTTCATCAGCTGCAG	58.8%	0	407.6	20	5190	188	25
QY	2140	ACCTTTGGCCAGAGTATCCCTCCCGTGCCTTCACATCCAGGGGCTTCACACAGATCCGG		0	1.6e-114				
QY	2158	GGCTGCTTGGGGAGGCACTG-----GAAAGATATGAGAGCCAGGG							
QY	2200	AGCTGATTTGGGGTGGCAGTGGAGACAGCTGGACAGCAGAGGTGTATGGAAACCCACGGA							
QY	2202	GAGACAAGGGGGCTTGAAGAAAGAAAGAGGGCAAAACAGGCCACACAGAGGGGCAGAG							
QY	2260	CAGAGAGGGGGGGCCCAAGGAAAG---GAGAGGGCAAAACAGGCCAGACCG--GGCCGAG							
QY	2262	CCGAGAACTGAGTTAACTCCTTCTTGTGTGCATCTTCCATAGAGAGCAGTGGAACTCTG							
QY	2315	CCCAAGAGCCAGGCTAACCCCTTCTCTTACTCTCTTCCCTTAGAGAG--GCAGGCACTGCC							
QY	2322	TGACCAACATCCCCCATGAGACCCCCACTACCCATACCAATTTGGCCTGAGTGCATTTCT							
QY	2373	TGCCCCACCCCTCAGCCCCCGCCCTTACACCTCTCCCAATTTGGTGTGCTCAGGGGCGCA							
QY	2382	AGGTTTC-CTGAGGAGCAGAGCCTGGCCTTGTGCTCTTGAACCTGAGCCCAAGCTGACCCAA							
QY	2433	GGGTTCTCCCGAAGACAAAGCCTGTGTCTTGTCACTGAGACCTTACCCAGGCTGACTTGG							
QY	2441	TGTTCTCAGTACCTTGTGAATGCCCTCAGAGCTTGAGAACCAAGCAGTGTACATATTAGGC							
QY	2493	TATTTTC-CAGCCCTTATCAGAGTCCCGAGGGGAGATGGGAAACAGGCACTGAGCAGCAGGC							
QY	2501	CATGGGCTAACCTCTGAGAGCTTGGACACAGAGAGCTCTCAAGTGAACCTCCAGGGACACACTG							
QY	2552	CAGGGGATTAACCC-CGAGCTTGTGACATGGGGGCTCTAAGTGAACCT-----AGACCTA							
QY	2561	CAGACAGGTGGGCTTTATCCCAAGAGCAACCATTTGGGATATGAGTGGCTGC--AAATG							
QY	2603	GAGACAGGTGGCTTGCATCCCTCTGAGGGCAACGGTTTGGCATGTGCACTTGCAGAGAGATG							
QY	2618	GGAATGCAAGTGTGAATCAGAGTCCCTTCAAGAAATCTACTGACATGCAAGAAGCCTTAAGACCCCTG							
QY	2663	GGATGGCCGGTCACTCAGAGTCCCTCTCAAGAGACCTGAGATCTGGGGTCCAAAGTCCCA							
QY	2678	GAGAGAGGGGTATGCTCTGCCCCCACCACCAATTAAGGGAGTGAACCTATCTTAGGGGGC							
QY	2723	GAGAGAGATGTGTCTCTGAGACCCCG-----TAATAGGCAGCCACATCTTAGGGGGC							
QY	2738	TGCGCAGCTTGGGGAGACAGCA--CATTACTGAGAGGTGAG--CCAGAAAACTGACC							
QY	2775	TGACAACTTGGGGGGAGAACCCCATCTTTCACAGGACAGTCTCCACCCAGAGAACTGACC							
QY	2795	GCCTGTGTCTGTGCCCACTTCCACACTCTAGAGCTATATTGAGAGGTGAGAGTATAGG							
QY	2835	CTGTGCTGTCTTACCCACCTTCCACACCTTGAAGTATATGAGAGGTGTCAGTGGATAGG							
QY	2855	GTCGAGACTGTATGACAGGAGAGTGTCTTGGGTGTGAGGGTGTGAGGGAAAGCCAGAGC							
QY	2895	G-GTGGAGGGGAGACTGAGCAGATATCTTGGGTGTGAGGGTGTGAGGGAAAGCCAGAGC							
QY	2915	AGGGAGTCTGTGCTTGTCTCTGAGACACAAATGTCTATAGTTATTAACAGGCATGACCT							
QY	2954	AGGAGATCTGGCTTTGTCTTCTGAGACAAATGTCTCTTAGTTCACAAAGGCAGGCCT							
QY	2975	GCTAAAGACCAACATCTACGACTCTGAAA--AGACAGAGCCCTGAGAGCAGGGGTT							
QY	3014	GTTGAAACCCGACACTTACCGCTCTGAGAGGGGACAGCTGTGAGATGTGATTAAGC							
QY	3033	GTCCTGAGCCCTTGGGTCTTGTATGTGTCACAAAGAGGGCATGATGTGATTAAGC							

Db 3074 ACCCTTGAGGGCTGGTCTTGAGAGACCCCTCCCAAGACAGGCACTGGAGAGTGAGGC 3133
Qy 3093 CCCGAGAGGCTTAGAGAGAGGAGCCTTGGAGAGGGGTCAGTCTGAGAGGCCCCATTCAT 3152
Db 3134 TCAGAGAGGAGATGACAGGCTTCTATCTGGAGAGGGGACAGCTACAGAGCCCCCTCCCC 3193
Qy 3153 GGAATCTGAGAGCCTGGGGCCAACTGTGTAAATCTCTGGGCTGGCCAGGATTCAAAGCA 3212
Db 3194 CAACCCCTGACACCCCTGTCAGAGCCCTGTGGAAACGAGAGCCAGGCCAATTGGTAAAT 3253
Qy 3213 GCACCTGTCATCTCTGTCAGAGCTTGGAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAG 3272
Db 3254 CCCCAGGCTGTCTGGGAGCCCGACCATCTCGGACACACCTGAGCCCTCTGGAGAGCTG 3313
Qy 3273 TTCTCCCTCAGCCCGAGATTAACACCTGAGCTGACCTTCCCTCCCTCCCATCAGCA 3332
Db 3314 GAGAGGCGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3373
Qy 3333 GTGAGAGGCTTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3392
Db 3374 GCAGAGGCTGGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3418
Qy 3393 ATGATCAATGATGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3452
Db 3419 GAGCATCGGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3472
Qy 3453 AAAGTGTGTGATGT 3512
Db 3473 -----TGTGATGT 3492
Qy 3513 GTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3572
Db 3493 AGTCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3552
Qy 3573 GTGATCCCTTCCATGCTTAAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 3632
Db 3553 GAGAAATTCCTTCCATGCTTAAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 3612
Qy 3633 AAATAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3692
Db 3613 GAAATGCTGGGGCTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3672
Qy 3693 CTTGTAGAGATGTGGGCAACAGAGCTACAGACAGTATCTGTACAGAGTAAAGAGAGA 3752
Db 3673 CTTGCC-----TGGAAATAGAGCCAGGACAGAGGAGTGTGAGAGGAGTGGGAGAGG 3724
Qy 3753 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3812
Db 3725 ACAAG-----AGGAAACTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3757
Qy 3813 TGGATGCTCTCCCTAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3872
Db 3758 TAGACGCTGCTCCAGCTCAGAG-----TCCA 3785
Qy 3873 GGTCTGAGAGAGTGAAGGCTCCCTCAGCCT-GAAGCTATGAGATAGCCAGGGTGA 3931
Db 3786 GGTCTGAGAGAGTGAAGGCTCCCTCAGCCTGAGGAGTGTGAGAGAGGAGGAGGAGGAG 3845
Qy 3932 AGGGGAGAGGAG-GAGCTGGAGTGAAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3990
Db 3846 TGGGAGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3905
Qy 3991 AGGCTGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4048
Db 3906 GTCTTAATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3965
Qy 4049 TAACTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4104
Db 3966 TAACTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4025
Qy 4105 CTGATGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4164

Db 4026 CTATCTGCCATCAGGCTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4085
Qy 4165 GGAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4216
Db 4086 GAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4137

RESULT 8
US-09-874-389-7
Sequence 7, Application US/09874389
Patent No. US20020152489A1
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
Goessen, Manfred
TITLE OF INVENTION: Animal Transgenic for a Tetracycline- Inducible Transcription
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/874,389
FILING DATE: 26-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/161,902
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/275,876
FILING DATE: 15-JULY-1994
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-94
APPLICATION NUMBER: US 08/260,452
FILING DATE: 14-JUNE-1994
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-1993
APPLICATION NUMBER: US 08/076,726
FILING DATE: 14-JUNE-1993
ATTORNEY/AGENT INFORMATION:
NAME: Decont, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BH1-009CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-874-389-7

Query Match 5.4%; Score 311.8; DB 9; Length 520;
Best Local Similarity 99.4%; Pred. No. 2,7e-85;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4277 GGAATCGAATTACCACTCCCTATCATGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4336
Db 63 GATCTCGAGTTTACCACTCCCTATCATGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 122
Qy 4337 TCCTATCATGATAG 4396

Db 123 TCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTTTACCACTCCCTATCAGTATAGAG 182
QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTT 4456
Db 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTT 242
QY 4457 TACCACTCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTTTACCACTCCCTATCAGT 4516
Db 243 TACCACTCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTTTACCACTCCCTATCAGT 302
QY 4517 ATAGAGAAAAGTGAAGTTCAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGT 4576
Db 303 ATAGAGAAAAGTGAAGTTCAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGT 362
QY 4577 CGAGCTCGGTACCG 4591
Db 363 CGAGCTCGGTACCG 377

RESULT 9
US-09-921-650-7
Sequence 7, Application US/09921650
Publication No. US2003022315A1
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
Goossen, Manfred
TITLE OF INVENTION: Tetracycline-Inducible Transcriptional
Activator Fusion Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/921,650
FILING DATE: 03-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/912,650
FILING DATE: 2001-08-03
APPLICATION NUMBER: US 08/485,978
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/383,754
FILING DATE: 03-FEB-1995
APPLICATION NUMBER: US 08/275,876
FILING DATE: 15-JULY-1994
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-1994
APPLICATION NUMBER: US 08/260,452
FILING DATE: 14-JUNE-1994
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-1993
APPLICATION NUMBER: US 08/076,726
FILING DATE: 14-JUNE-1993
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-0096CNDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-921-650-7
Query Match
Best Local Similarity 99.4%; Score 311.8; DB 10; Length 520;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4277 GGAAGTTCAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTTTACCA 4336
Db 63 GGATCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTTTACCA 122
QY 4337 TCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTTTACCACTCCCTATCAGTATAGAG 4396
Db 123 TCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTTTACCACTCCCTATCAGTATAGAG 182
QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTT 4456
Db 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTT 242
QY 4457 TACCACTCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTTTACCACTCCCTATCAGT 4516
Db 243 TACCACTCCCTATCAGTATAGAGAAAAGTGAAGTTCAGTTTACCACTCCCTATCAGT 302
QY 4517 ATAGAGAAAAGTGAAGTTCAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGT 4576
Db 303 ATAGAGAAAAGTGAAGTTCAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGT 362
QY 4577 CGAGCTCGGTACCG 4591
Db 363 CGAGCTCGGTACCG 377

RESULT 10
US-09-241-347-7
Sequence 7, Application US/09241347
Publication No. US20040003417A1
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
Goossen, Manfred
TITLE OF INVENTION: Animals Transgenic for a Tetracycline-
Controlled Transc
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/241,347
FILING DATE: 02-Feb-1999
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,814
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/383,754
FILING DATE: 03-FEB-1995
APPLICATION NUMBER: US 08/275,876
FILING DATE: 15-JULY-1994
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-1994
APPLICATION NUMBER: US 08/260,452
FILING DATE: 14-JUNE-1994
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-1993

Query Match	5.4%	Score 311.8;	DB 11;	Length 520;
Best Local Similarity	99.4%;	Pred. No. 2.7e-85;		
Matches 313;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

```

RESULT 11
US-10-134-643-17
Sequence 17, Application US/10134643
Publication No. US20030111898A1
GENERAL INFORMATION:
APPLICANT: OLSEN, JOHN C.
APPLICANT: MITROPHANOUS, KYRIACOS ANDREOU
APPLICANT: ROHILL, JONATHAN
APPLICANT: KINGSMAN, ALAN JOHN
APPLICANT: ELIARD, FIONA MARGARET
TITLE OF INVENTION: METHODS FOR PRODUCING HIGH TITRE VECTORS AND
TITLE OF INVENTION: COMPOSITIONS USED IN SUCH METHODS
FILE REFERENCE: 078883-0148
CURRENT APPLICATION NUMBER: US/10/134,643
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/287,048
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 990
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

```

Query Match	5.4%;	Score 311.4;	DB 15,	Length 950;
Best Local Similarity	99.7%;	Pred. No. 5.1e-85;		
Matches 312; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

RESULT 12
US-10-102-143-12/c

Query Match	5.4%	Score 311;	DB 16;	Length 4438;
Best Local Similarity	96.9%	Pred. No. 1.5e-84;		
Matches 317; Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0;

Qy	4263	CTAACGACAGAGAGAACTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTAAA	4322
Db	979	CTTATCGATACCGTGACCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTAAA	920
Qy	4323	GTCCAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTCAGTTTACCACTCC	4382
Db	919	GTCCAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTCAGTTTACCACTCC	860
Qy	4383	TATCAGTATAGAGAAAAGTCAGTTTACCACTCCCTATCAGTGATAGAGAAA	4442
Db	859	TATCAGTATAGAGAAAAGTCAGTTTACCACTCCCTATCAGTGATAGAGAAA	800

```
QY 4443 GTGAAGTCAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACC 4502
|||
DB 799 GTGAAGTCAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACC 740
|||
QY 4503 ACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATAG 4562
|||
DB 739 ACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATAG 680
|||
QY 4563 AGAAAAGTGAAGTCAGTCCGCTACC 4589
|||
DB 679 AGAAAAGTGAAGTCAGTCCGCTACC 653
|||
```

RESULT 13

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US-10-102-143-10/c
; Sequence 10, Application US/10102143
; Publication No. US20030185851A1
; GENERAL INFORMATION:
; APPLICANT: Soldati, Dominique
; APPLICANT: Meisner, Markus
; TITLE OF INVENTION: TET transactivator system
; FILE REFERENCE: 04630/016001
; CURRENT APPLICATION NUMBER: US/10/102,143
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 4479
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1193)..(1924)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1102)
; OTHER INFORMATION: n is disclosed as an asterisk
; OTHER INFORMATION: Description of Artificial Sequence: pTetO7Sag1-GFP
US-10-102-143-10
```

```
Query Match 5.4%; Score 311; DB 16; Length 4479;
Best Local Similarity 96.9%; Pred. No. 1.5e-84;
Matches 317; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 4263 CTAAACGACGAGGAGAACTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGA 4322
|||
DB 979 CTATCGATACCGTCGACCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGA 920
|||
QY 4323 GTGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCC 4382
|||
DB 919 GTGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCC 860
|||
QY 4383 TATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATAGAGAAA 4442
|||
DB 859 TATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATAGAGAAA 800
|||
QY 4443 GTGAAGTCAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACC 4502
|||
DB 799 GTGAAGTCAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACC 740
|||
QY 4503 ACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATAG 4562
|||
DB 739 ACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATAG 680
|||
QY 4563 AGAAAAGTGAAGTCAGTCCGCTACC 4589
|||
DB 679 AGAAAAGTGAAGTCAGTCCGCTACC 653
|||
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RESULT 14
US-10-102-143-8/c
; Sequence 8, Application US/10102143
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```
; Publication No. US20030185851A1
; GENERAL INFORMATION:
; APPLICANT: Soldati, Dominique
; APPLICANT: Meisner, Markus
; TITLE OF INVENTION: TET transactivator system
; FILE REFERENCE: 04630/016001
; CURRENT APPLICATION NUMBER: US/10/102,143
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 4556
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1270)..(2001)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pTetO7Sag1-GFP
US-10-102-143-8
```

```
Query Match 5.4%; Score 311; DB 16; Length 4556;
Best Local Similarity 96.9%; Pred. No. 1.5e-84;
Matches 317; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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```
QY 4263 CTAAACGACGAGGAGAACTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGA 4322
|||
DB 979 CTATCGATACCGTCGACCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGA 920
|||
QY 4323 GTGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCC 4382
|||
DB 919 GTGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCC 860
|||
QY 4383 TATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATAGAGAAA 4442
|||
DB 859 TATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATAGAGAAA 800
|||
QY 4443 GTGAAGTCAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACC 4502
|||
DB 799 GTGAAGTCAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACC 740
|||
QY 4503 ACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATAG 4562
|||
DB 739 ACTCCCTATCAGTATAGAGAAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATAG 680
|||
QY 4563 AGAAAAGTGAAGTCAGTCCGCTACC 4589
|||
DB 679 AGAAAAGTGAAGTCAGTCCGCTACC 653
|||
```

```
RESULT 15
US-10-102-143-6/c
; Sequence 6, Application US/10102143
; Publication No. US20030185851A1
; GENERAL INFORMATION:
; APPLICANT: Soldati, Dominique
; APPLICANT: Meisner, Markus
; TITLE OF INVENTION: TET transactivator system
; FILE REFERENCE: 04630/016001
; CURRENT APPLICATION NUMBER: US/10/102,143
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1193)..(3787)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1102)
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; OTHER INFORMATION: n is disclosed as an asterisk
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pterc075ag1-MyoA
US-10-102-143-6

Query Match 5.4%; Score 311; DB 16; Length 6346;
Best Local Similarity 96.9%; Pred. No. 1.8e-84;
Matches 317; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	4263	CTAACGACACGAGGAACTCGAGTTTACCACTCCCTATCATGATGATAGAGAAAGTGAAA	4322
Db	979	CTTATCGATACCGTCGACCTCGAGTTTACCACTCCCTATCATGATGATAGAGAAAGTGAAA	920
QY	4323	GTCGAGTTTACCACTCCCTATCATGATGATAGAGAAAGTGAAAGTCGAGTTTACCCTCCC	4382
Db	919	GTCGAGTTTACCACTCCCTATCATGATGATAGAGAAAGTGAAAGTCGAGTTTACCCTCCC	860
QY	4383	TATCAGTATAGAGAAAGTGAAAGTCGAGTTTACCACTCCCTATCATGATGATAGAGAAA	4442
Db	859	TATCAGTATAGAGAAAGTGAAAGTCGAGTTTACCACTCCCTATCATGATGATAGAGAAA	800
QY	4443	GTCGAAAGTCGAGTTTACCACTCCCTATCATGATGATAGAGAAAGTGAAAGTCGAGTTTACC	4502
Db	799	GTCGAAAGTCGAGTTTACCACTCCCTATCATGATGATAGAGAAAGTGAAAGTCGAGTTTACC	740
QY	4503	ACTCCCTATCATGATGATAGAGAAAGTGAAAGTCGAGTTTACCACTCCCTATCATGATGATAG	4562
Db	739	ACTCCCTATCATGATGATAGAGAAAGTGAAAGTCGAGTTTACCACTCCCTATCATGATGATAG	680
QY	4563	AGAAAGTGAAAGTCGAGCTCGGTACC	4589
Db	679	AGAAAGTGAAAGTCGAGCTCGGTACC	653

Search completed: August 30, 2005, 09:27:53
Job time : 2396 secs

Query March	22.3%	Score 1279.8	DB 2;	length 1679;
Best Local Similarity	82.2%	Pred. No. 0;		
Matches 1616; Conservative	0;	Mismatches 57;	Indels 292;	Gaps 1,

QY 3767 GAATTCCTTACTATCAAAAGGAAACTAGTCGTGACCTGCAAAAGTGATGCTCCCT 3826
Db 1 GAATTCCTTACTATCAAAAGGAAACTAGTCGTGACCTGCAAAAGTGATGCTCCCT 60
QY 3827 AGACATATATGATTTGCTCTCTGGGAGACCACTGTGGAACTTCAAGTCTGAGAGATA 3886
Db 61 AGACATATATGATTTGCTCTGGGAGACCACTGTGGAACTTCAAGTCTGAGAGATA 120
QY 3887 GGAAGCTCCCTCAGCCTGAAGCTATGACATGACGAGGTTGAAAAGGAGAGAG 3946
Db 121 GGAAGCTCCCTCAGCCTGAAGCTATGACATGACGAGGTTGAAAAGGAGAGAG 180
QY 3947 CTTGGATGAGAGCTGTGTGTGGAGCAAGGAGAGATATTAAGCTGAAAGAGAG 4006
Db 181 CTTGGATGAGAGCTGTGTGTGGAGCAAGGAGAGATATTAAGCTGAAAGAGAG 240
QY 4007 TGACCTTACCCAGTTTGTCAACTCACTCCCTTCAATTTAAATTAACCTGAAGTAAAGGCT 4066
Db 241 TGACCTTACCCAGTTTGTCAACTCACTCCCTTCAATTTAAATTAACCTGAAGTAAAGGCT 300
QY 4067 GGGTAAAGGAGGTGTGTGAGACGCTCTGTCTCTCTGATGATGCAATGCAAGAACTGCAAT 4126
Db 301 GGGTAAAGGAGGTGTGTGAGACGCTCTGTCTCTCTGATGATGCAATGCAAGAACTGCAAT 360
QY 4127 GGGAGAGAAATGTGCCAAGACTTAAAGGCAATGAGCCAGAGGGGCGAGAGCAA 4186
Db 361 GGGAGAGAAATGTGCCAAGACTTAAAGGCAATGAGCCAGAGGGGCGAGAGCAA 420
QY 4187 CAGACCTTTTCAATGGGCAAACTTGGGGCCGTGATGATGCAATGCAAGAACTGCAAT 4246
Db 421 CAGACCTTTTCAATGGGCAAACTTGGGGCCGTGATGATGCAATGCAAGAACTGCAAT 480
QY 4247 CGATACCTTCTTCTTCAACGAGAGGAACTGAGTTTACCACTCCCTATCAGTG 4306
Db 481 CGATACCTTCTTCTTCAACGAGAGGAACTGAGTTTACCACTCCCTATCAGTG 525
QY 4307 ATAGAGAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATGAGAAAGTGAAGT 4366
Db 525 ATAGAGAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATGAGAAAGTGAAGT 525
QY 4367 CGAGTTTACCACTCCCTATCAGTATGAGAAAGTGAAGTGAAGTTTACCACTCCCTA 4426
Db 525 CGAGTTTACCACTCCCTATCAGTATGAGAAAGTGAAGTGAAGTTTACCACTCCCTA 525
QY 4427 TCAATGATAGAGAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATGAGAAAGT 4486
Db 525 TCAATGATAGAGAAAGTGAAGTCAGTTTACCACTCCCTATCAGTATGAGAAAGT 525
QY 4487 GAAAGTCAGTTTACCACTCCCTATCAGTATGAGAAAGTGAAGTCAGTTTACCACT 4546
Db 525 GAAAGTCAGTTTACCACTCCCTATCAGTATGAGAAAGTGAAGTCAGTTTACCACT 525
QY 4547 TCCCTATCAGTATGAGAAAGTGAAGTCAGTATGAGAAAGTGAAGTCAGTATGAGAA 4606
Db 525 TCCCTATCAGTATGAGAAAGTGAAGTCAGTATGAGAAAGTGAAGTCAGTATGAGAA 548
QY 4607 TTAGGAGAGAGATATGAGATGAGATATTAAGGAGCTGAGAGCTGAGAGCTGAGAG 4666
Db 549 TTAGGAGAGAGATATGAGATGAGATATTAAGGAGCTGAGAGCTGAGAGCTGAGAG 608
QY 4667 ATTTCTCAACCCAGATGAGAGAGATTTGGGAGGCTCTTCAACCCAGAGAGCT 4726
Db 609 ATTTCTCAACCCAGATGAGAGAGATTTGGGAGGCTCTTCAACCCAGAGAGCT 668
QY 4727 CTCCCACTGAAGAAAGTGCCTTCCCTGAGATGGGGTTCAAGCCGCTCAAGATCT 4786
Db 669 CTCCCACTGAAGAAAGTGCCTTCCCTGAGATGGGGTTCAAGCCGCTCAAGATCT 728
QY 4787 GACAGAGGTGCTTCAACAGAGCTGAGAGATTTCTCAGTGTGAGAGAGTTTCAAGAAA 4846
Db 729 GACAGAGGTGCTTCAACAGAGCTGAGAGATTTCTCAGTGTGAGAGAGTTTCAAGAAA 788
QY 4847 CACTGATGCTCCCTTCCCTTACGCTGTCTTCTCACTTCTCTGAGGAGTGTCTCTCC 4906

Db 789 CACTGATGCTCCCTTCCCTTACGCTGTCTTCTCACTTCTCTGAGGAGTGTCTCTCC 848
QY 4907 CGCTTGTGTTATTCCTGAGCTCTTCCCTTCAAGAGATTTGGCCCTGAGCTCACTCA 4966
Db 849 CGCTTGTGTTATTCCTGAGCTCTTCCCTTCAAGAGATTTGGCCCTGAGCTCACTCA 908
QY 4967 TCTTCTCTACTGTCTCCGAGCTTTCCTTGCCTTCTGCTGCTCTTCTTCAACCA 5026
Db 909 TCTTCTCTACTGTCTCCGAGCTTTCCTTGCCTTCTGCTGCTCTTCTTCAACCA 968
QY 5027 TTTCTCACTTCACTTTTCTCCCTTCTCAATTTGATTTATCTTCTTCTTCTTCT 5086
Db 969 TTTCTCACTTCACTTTTCTCCCTTCTCAATTTGATTTATCTTCTTCTTCTTCT 1028
QY 5087 TCCCTCTTCT 5146
Db 1029 TCCCTCTTCT 1088
QY 5147 TCCCTCTTCT 5206
Db 1089 TCCCTCTTCT 1148
QY 5207 TAAACATCTTCCAGTGTGAGCCAGACTTCACTGTCTGTGTGTCTTCTTCTCTCA 5266
Db 1149 TAAACATCTTCCAGTGTGAGCCAGACTTCACTGTCTGTGTGTCTTCTTCTCTCA 1208
QY 5267 CCCCCTGAGTGTCT 5326
Db 1209 CCCCCTGAGTGTCT 1268
QY 5327 CTACT 5386
Db 1269 CTACT 1328
QY 5387 CAGCTGTGTCTCACTTTCTTCAAGATTTCTGTGAAAAGTTTAAACAGGTGAGAA 5446
Db 1329 CAGCTGTGTCTCACTTTCTTCAAGATTTCTGTGAAAAGTTTAAACAGGTGAGAA 1388
QY 5447 CTGTAGACAGAGATATCAGATTTCTCCGGAAGTCAGAGCTTCCAGCTCTCTTCTCTG 5506
Db 1389 CTGTAGACAGAGATATCAGATTTCTCCGGAAGTCAGAGCTTCCAGCTCTCTTCTCTG 1448
QY 5507 CCAGCTGCCCGGACCTTTAGCAAACTTCAAGGACCTTTAACCACATAGACCTGTGACA 5566
Db 1449 CCAGCTGCCCGGACCTTTAGCAAACTTCAAGGACCTTTAACCACATAGACCTGTGACA 1508
QY 5567 GAGAGCAGGACCTTTTACATGAGTCTGTGTGAGAGAGCCATAGGCTTACGTTTAAAGA 5626
Db 1509 GAGAGCAGGACCTTTTACATGAGTCTGTGTGAGAGAGCCATAGGCTTACGTTTAAAGA 1568
QY 5627 GGCAGGAAAGTGTGTGTGAGAAAGTCAGAGCTTCAATAGAGCTTACCCACACAG 5686
Db 1569 GGCAGGAAAGTGTGTGTGAGAAAGTCAGAGCTTCAATAGAGCTTACCCACACAG 1628
QY 5687 AAATGACAGACAGATCCCTCTATCTTCCCATTAAGAGTTTGAAT 5731
Db 1629 AAATGACAGACAGATCCCTCTATCTTCCCATTAAGAGTTTGAAT 1673

RESULT 2
US-08-880-342-11
; Sequence 11, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopton, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 37

QY 5267 CCCCCTGGCTTGTCTGTTCCATCTGCTGAGATCTCTAGATTGCTCTCCAGCCTCTG 5326
DB 1209 CCCCCTGGCTTGTCTGTTCCATCTGCTGAGATCTCTAGATTGCTCTCCAGCCTCTG 1268
QY 5327 CTACTCTCTTCTGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5386
DB 1269 CTACTCTCTTCTGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328
QY 5387 CAGCTGTGTCTCAACATCTTCAAGATCTCTGAAAAAGTTAAACAGAGTGAATGTTTCC 5446
DB 1329 CAGCTGTGTCTCAACATCTTCAAGATCTCTGAAAAAGTTAAACAGAGTGAATGTTTCC 1388
QY 5447 CTGTAGACAGACAGATCAAGATCTCTCCGAAATGACAGCTCTCTCTCTCTCTG 5506
DB 1389 CTGTAGACAGACAGATCAAGATCTCTCCGAAATGACAGCTCTCTCTCTCTCTG 1448
QY 5507 CCGCTCTCCGCGCACTTCTGAGAACTCAAGGACCTTACCCCACTAGACCTCTGACA 5566
DB 1449 CCGCTCTCCGCGCACTTCTGAGAACTCAAGGACCTTACCCCACTAGACCTCTGACA 1508
QY 5567 GAGAGGAGGACATCTTACATGAGAGCTGCTGAGGAGGACCATAGAGCTAGCTGTAAGA 5626
DB 1509 GAGAGGAGGACATCTTACATGAGAGCTGCTGAGGAGGACCATAGAGCTAGCTGTAAGA 1568
QY 5627 GCGAGGAAAGTGTGTGTAGAGAAAGTCAAGACTTCAATAGAAAGCTAGCCCAACAG 5686
DB 1569 GCGAGGAAAGTGTGTGTAGAGAAAGTCAAGACTTCAATAGAAAGCTAGCCCAACAG 1628
QY 5687 AAATGACAGACAGATCCCTCTATCTCCCATAGAGTTGAGT 5731
DB 1629 AAATGACAGACAGATCCCTCTATCTCCCATAGAGTTGAGT 1673

RESULT 3

US-09-376-774-5
Sequence 5, Application US/09376774
Patent No. 6759236
GENERAL INFORMATION:
APPLICANT: Fung, Yuen Kai
APPLICANT: Gomer, Charles
APPLICANT: T'Ang, Anne
TITLE OF INVENTION: Methods To Enhance And Confine Expression
TITLE OF INVENTION: Of Genes
FILE REFERENCE: D6087
CURRENT APPLICATION NUMBER: US/09/376, 774
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/096,947
PRIOR FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 5
LENGTH: 10728
TYPE: DNA
ORGANISM: Unknown
FEATURES:
NAME/KEY: misc_feature
OTHER INFORMATION: recombinant vector pDATM-TNF?
US-09-376-774-5

Query Match 5.5%; Score 312.6; DB 4; Length 10728;
Best Local Similarity 97.2%; Pred. No. 7.7e-82;
Matches 318; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4265 AACGACAGAGGAGAACTCGATTACCACTCCCTATCAGTATAGAGAAAAAGTGAAGT 4324
DB 212 ATCCGACAGAGAGCTGTGCGAGTTTACCACTCCCTATCAGTATAGAGAAAAAGTGAAGT 271
QY 4325 CGAGTTTACCACTCCCTATCAGTATAGAGAAAAAGTGAAGTGAAGTTTACCACTCCCTA 4384
DB 272 CGAGTTTACCACTCCCTATCAGTATAGAGAAAAAGTGAAGTGAAGTTTACCACTCCCTA 331
QY 4385 TCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAAGT 4444
DB 332 TCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAAGT 391

QY 4445 GAAAGTCGATTATACCACTCCCTATCAGTATAGAGAAAAAGTGAAGTGAAGTTTACCA 4504
DB 392 GAAAGTCGATTATACCACTCCCTATCAGTATAGAGAAAAAGTGAAGTGAAGTTTACCA 451
QY 4505 TCCTTATCAGTATAGAGAAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4564
DB 452 TCCTTATCAGTATAGAGAAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 511
QY 4565 AAAAGTGAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4591
DB 512 AAAAGTGAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 538

RESULT 4

US-08-485-971-7
Sequence 7, Application US/08485971
Patent No. 5589362
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
APPLICANT: Gossen, Manfred
APPLICANT: Hillen, Wolfgang
APPLICANT: Hehl, Vera
APPLICANT: Schnappinger, Dirk
TITLE OF INVENTION: Tetracycline-Regulated Transcriptional
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,971
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/383,754
FILING DATE: 03-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,452
FILING DATE: 14-JUNE-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,726
FILING DATE: 14-JUNE-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deconci, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-009CP7
TELEPHONE: (617)227-5941
TELEFAX: (617)227-7400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-485-971-7

Query Match 5.4%; Score 311.8; DB 1; Length 520;

Best Local Similarity 99.4%; Pred. No. 1.7e-82;

Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4277 GGAACCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCAAC 4336
DB 63 GGATCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCAAC 122
QY 4337 TCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4396
DB 123 TCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 182
QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTT 4456
DB 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTT 242
QY 4457 TACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTG 4516
DB 243 TACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTG 302
QY 4517 ATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGT 4576
DB 303 ATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGT 362
QY 4577 CGAGCTCGGTACCAG 4591
DB 363 CGAGCTCGGTACCAG 377

RESULT 5

US-08-275-876-7

Sequence 7, Application US/08275876

Patent No. 5654168

GENERAL INFORMATION:

APPLICANT: Bujard, Hermann

APPLICANT: Gossen, Manfred

TITLE OF INVENTION: Tetracycline-Inducible Transcriptional

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESSES:

ADDRESSEE: LAHYE & COCKFIELD

STREET: 60 State Street, suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/275,876

FILING DATE:

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US

FILING DATE: 01-JULY-94

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A. Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BBI-009CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 520 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-275-876-7

Query Match 5.4%; Score 311.8; DB 1; Length 520;

Best Local Similarity 99.4%; Pred. No. 1.7e-82;

Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4277 GGAACCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCAAC 4336
DB 63 GGATCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCAAC 122
QY 4337 TCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4396
DB 123 TCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 182
QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTT 4456
DB 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTT 242
QY 4457 TACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTG 4516
DB 243 TACCACTCCCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTG 302
QY 4517 ATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGT 4576
DB 303 ATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAGT 362
QY 4577 CGAGCTCGGTACCAG 4591
DB 363 CGAGCTCGGTACCAG 377

RESULT 6

US-08-383-754-7

Sequence 7, Application US/08383754

Patent No. 5789156

GENERAL INFORMATION:

APPLICANT: Bujard, Hermann

APPLICANT: Gossen, Manfred

TITLE OF INVENTION: Tetracycline-Regulated Transcriptional

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESSES:

ADDRESSEE: LAHYE & COCKFIELD

STREET: 60 State Street, suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/383,754

FILING DATE:

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/275,876

FILING DATE: 15-JULY-94

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/270,637

FILING DATE: 01-JULY-94

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,452

FILING DATE: 14-JUNE-94

CLASSIFICATION: 436

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-93
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,726
FILING DATE: 14-JUNE-93
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: DeConci, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-383-754-7
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Query Match 5.4%; Score 311.8; DB 1; Length 520;
Best Local Similarity 99.4%; Pred. No. 1.7e-82;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 4277 GGAAGTGAATTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4336
DB 63 GGATCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4336
QY 4337 TCCTATCAGTATAGAGAAAGTGAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4396
DB 123 TCCTATCAGTATAGAGAAAGTGAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4396
QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4456
DB 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4456
QY 4457 TACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4516
DB 243 TACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4516
QY 4517 ATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4576
DB 303 ATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4576
QY 4577 CGAGCTCGTACCG 4591
DB 363 CGAGCTCGTACCG 377
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RESULT 7
US-08-485-978-7
Sequence 7, Application US/08485978
Patent No. 5814618
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
APPLICANT: Gossen, Manfred
TITLE OF INVENTION: Methods for Regulating Gene Expression
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,978
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/383,754
FILING DATE: 03-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,876
FILING DATE: 15-JULY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,452
FILING DATE: 14-JUNE-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,726
FILING DATE: 14-JUNE-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeConci, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-009CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-485-978-7
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Query Match 5.4%; Score 311.8; DB 1; Length 520;
Best Local Similarity 99.4%; Pred. No. 1.7e-82;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 4277 GGAAGTGAATTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4336
DB 63 GGATCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4336
QY 4337 TCCTATCAGTATAGAGAAAGTGAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4396
DB 123 TCCTATCAGTATAGAGAAAGTGAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4396
QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4456
DB 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4456
QY 4457 TACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4516
DB 243 TACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4516
QY 4517 ATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4576
DB 303 ATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAG 4576
QY 4577 CGAGCTCGTACCG 4591
DB 363 CGAGCTCGTACCG 377
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RESULT 8
US-08-486-814-7
Sequence 7, Application US/08486814
Patent No. 5865755
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
TITLE OF INVENTION: Animals Transgenic for a Tetracycline-
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,814
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/383,754
FILING DATE: 03-FEB-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,876
FILING DATE: 15-JULY-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,452
FILING DATE: 14-JUNE-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,726
FILING DATE: 14-JUNE-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Decont, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-009CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-486-814-7

Query Match 5.4%; Score 311.8; DB 2; Length 520;
Best Local Similarity 99.4%; Pred. No. 1.7e-82;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4277 GGAATCGAGTTTACCACTCCCTATAGATGATGAGAAAGTGAAGTGAAGTTTACCCAC 4336
DB 63 GGAATCGAGTTTACCACTCCCTATAGATGATGAGAAAGTGAAGTGAAGTTTACCCAC 122

QY 4337 TCCCTATCAGTATGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAG 4396
DB 123 TCCCTATCAGTATGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAG 182
QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAGTGAAGTGAAGTT 4456
DB 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAGTGAAGTGAAGTT 242
QY 4457 TACCACTCCCTATCAGTATGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTG 4516
DB 243 TACCACTCCCTATCAGTATGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTG 302
QY 4517 ATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAGTGAAGTT 4576
DB 303 ATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAGTGAAGTT 362
QY 4577 CGAGCTCGGTACCG 4591
DB 363 CGAGCTCGGTACCG 377

RESULT 9
US-08-487-472-7
Sequence 7, Application US/08487472
Patent No. 5912411
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
TITLE OF INVENTION: Animal Transgenic for a Tetracycline- Inducible Transcription
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,472
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/383,754
FILING DATE: 03-FEB-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,876
FILING DATE: 15-JULY-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-94
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,452
FILING DATE: 14-JUNE-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,726
FILING DATE: 14-JUNE-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Decont, Giulio A. Jr.

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/
/ REGISTRATION NUMBER: 31,503
/ REFERENCE/DOCKET NUMBER: BBI-009CP3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)227-5941
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 520 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-08-487-472-7

Query Match          5.4%; Score 311.8; DB 2; Length 520;
Best Local Similarity 99.4%; Pred. No. 1,7e-82;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4277 GGAAGTGGAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACAC 4336
Db 63 GGAATCTGAGATTTCACACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACAC 122
QY 4337 TCCTTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAG 4396
Db 123 TCCTTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAG 182
QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTT 4456
Db 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTT 242
QY 4457 TACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGT 4516
Db 243 TACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGT 302
QY 4517 ATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGT 4576
Db 303 ATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGT 362
QY 4577 CGAGCTCGGTACCG 4591
Db 363 CGAGCTCGGTACCG 377

RESULT 10
US-08-485-740-7
/ Sequence 7, Application US/08485740
/ Patent No. 6004941
/ GENERAL INFORMATION:
/ APPLICANT: Bujard, Hermann
/ APPLICANT: Gossen, Manfred
/ TITLE OF INVENTION: Methods for Regulating Gene Expression
/ NUMBER OF SEQUENCES: 28
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ STREET: 60 State Street, Suite 510
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485,740
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/383,754
/ FILING DATE: 03-FEB-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
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/
/ APPLICATION NUMBER: US 08/275,876
/ FILING DATE: 15-JULY-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/270,637
/ FILING DATE: 01-JULY-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/260,452
/ FILING DATE: 14-JUNE-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/076,327
/ FILING DATE: 14-JUNE-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/076,726
/ FILING DATE: 14-JUNE-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DeConti, Giulio A. Jr.
/ REGISTRATION NUMBER: 31,503
/ REFERENCE/DOCKET NUMBER: BBI-009CP5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)227-5941
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 520 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-08-485-740-7

Query Match          5.4%; Score 311.8; DB 3; Length 520;
Best Local Similarity 99.4%; Pred. No. 1,7e-82;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4277 GGAAGTGGAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACAC 4336
Db 63 GGAATCTGAGATTTCACACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACAC 122
QY 4337 TCCTTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAG 4396
Db 123 TCCTTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAG 182
QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTT 4456
Db 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTT 242
QY 4457 TACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGT 4516
Db 243 TACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGT 302
QY 4517 ATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGT 4576
Db 303 ATAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGT 362
QY 4577 CGAGCTCGGTACCG 4591
Db 363 CGAGCTCGGTACCG 377

RESULT 11
US-09-162-184-7
/ Sequence 7, Application US/09162184A
/ Patent No. 6136954
/ GENERAL INFORMATION:
/ APPLICANT: Bujard, Hermann
/ APPLICANT: Gossen, Manfred
/ TITLE OF INVENTION: Retriacycline-Inducible Transcriptional
/ Activator Fusion Proteins
```

NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,184A
FILING DATE: 28-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/383,754
FILING DATE: 03-FEB-1995
APPLICATION NUMBER: US 08/275,876
FILING DATE: 15-JULY-1994
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-1994
APPLICATION NUMBER: US 08/260,452
FILING DATE: 14-JUNE-1994
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-1993
APPLICATION NUMBER: US 08/076,726
FILING DATE: 14-JUNE-1993
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-009C6CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-162-184-7
Query Match 5.4%; Score 311.8; DB 3; Length 520;
Best Local Similarity 99.4%; Pred. No. 1,7e-82;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 363 CGAGCTCGGTACCCG 377
RESULT 12
US-09-161-902-7
Sequence 7, Application US/09161902
Patent No. 6242667
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
APPLICANT: Gossen, Manfred
TITLE OF INVENTION: Animal Transgenic for a Tetracycline- Inducible Transcription
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/161,902
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,472
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,876
FILING DATE: 15-JULY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-94
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,452
FILING DATE: 14-JUNE-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,726
FILING DATE: 14-JUNE-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-009CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-5941
TELEFAX: (617)227-7400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-161-902-7
Query Match 5.4%; Score 311.8; DB 3; Length 520;
Best Local Similarity 99.4%; Pred. No. 1,7e-82;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 63 GGAATCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 122
Qy 4337 TCCCTATCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 4396
Db 123 TCCCTATCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 182
Qy 4397 AAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 4456
Db 183 AAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 242
Qy 4457 TACCACTCCCTATCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 4516
Db 243 TACCACTCCCTATCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 302
Qy 4517 ATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 4576
Db 303 ATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 362
Qy 4577 CGAGCTCGGTACCG 4591
Db 363 CGAGCTCGGTACCG 377

RESULT 13
US-09-489-777A-7
Sequence 7, Application US/09489777A
Patent No. 6271348

GENERAL INFORMATION:

APPLICANT: Bujard, Hermann
Gossen, Manfred
TITLE OF INVENTION: Tetracycline-Inducible Transcriptional
Inhibitor Fusion Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,777A
FILING DATE: 24-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/162,184
FILING DATE: 28-SEP-1998
APPLICATION NUMBER: US 08/485,978
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/383,754
FILING DATE: 03-FEB-1995
APPLICATION NUMBER: US 08/270,637
FILING DATE: 15-JULY-1994
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-1994
APPLICATION NUMBER: US 08/260,452
FILING DATE: 14-JUNE-1994
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-1993
APPLICATION NUMBER: US 08/076,726
FILING DATE: 14-JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-009C6CNDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-489-777A-7

Query Match 5.4%; Score 311.8; DB 3; Length 520;
Best Local Similarity 99.4%; Fred. No. 1.7e-82;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4277 GGAATCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 4336
Db 63 GGAATCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 122
Qy 4337 TCCCTATCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 4396
Db 123 TCCCTATCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 182
Qy 4397 AAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 4456
Db 183 AAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 242
Qy 4457 TACCACTCCCTATCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 4516
Db 243 TACCACTCCCTATCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 302
Qy 4517 ATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 4576
Db 303 ATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTATAGAGAAAGTGAAGTTCAGTTTACAC 362
Qy 4577 CGAGCTCGGTACCG 4591
Db 363 CGAGCTCGGTACCG 377

RESULT 14
PCT-US95-08179-7
Sequence 7, Application PC/TUS9508179

GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Tetracycline-Regulated Transcriptional
Inhibitor Fusion Proteins
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08179
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: To be assigned
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/383,754
FILING DATE: 03-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:

NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-009C6CNDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400

APPLICATION NUMBER: US 08/275,876
FILING DATE: 15-JULY-94
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-94
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-009C2PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-08179-7

Query Match 5.4%; Score 311.8; DB 5; Length 520;
Best Local Similarity 99.4%; Pred. No. 1.7e-82;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4277 GGAACCTCGATTACCACTCCCTATCAGTATGAGAAAAGTGAAGTTCACAC 4336
DB 63 GGATCTCGATTACCACTCCCTATCAGTATGAGAAAAGTGAAGTTCACAC 122
QY 4337 TCCCTATCAGTATGAGAAAAGTGAAGTTCACCTCCCTATCAGTATGAG 4396
DB 123 TCCCTATCAGTATGAGAAAAGTGAAGTTCACCTCCCTATCAGTATGAG 182
QY 4397 AAAAGTGAAGTTCACCACTCCCTATCAGTATGAGAAAAGTGAAGTTCAGTT 4456
DB 183 AAAAGTGAAGTTCACCACTCCCTATCAGTATGAGAAAAGTGAAGTTCAGTT 242
QY 4457 TACCACTCCCTATCAGTATGAGAAAAGTGAAGTTCACCTCCCTATCAGTTG 4516
DB 243 TACCACTCCCTATCAGTATGAGAAAAGTGAAGTTCACCTCCCTATCAGTTG 302
QY 4517 ATGAGAAAAGTGAAGTTCACCTCCCTATCAGTATGAGAAAAGTGAAGTTCAGTT 4576
DB 303 ATGAGAAAAGTGAAGTTCACCTCCCTATCAGTATGAGAAAAGTGAAGTTCAGTT 362
QY 4577 CGAGCTCGTACCGAG 4591
DB 363 CGAGCTCGTACCGAG 377

RESULT 15
US-08-076-726-13/c
Sequence 13, Application US/08076726
Patent No. 5464758
GENERAL INFORMATION:
APPLICANT: Gossen, Manfred
APPLICANT: Bujard, Hermann
TITLE OF INVENTION: Tight Control of Gene Expression in
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSES: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: District of Columbia
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,726
FILING DATE: 14-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bemdond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.2490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
TELEX: 248636 SSX
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-076-726-13

Query Match 5.4%; Score 310.4; DB 1; Length 450;
Best Local Similarity 99.7%; Pred. No. 4.1e-82;
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4280 ACTCGAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTTCACCTCC 4339
DB 325 ACTCGAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTTCACCTCC 266
QY 4340 CTATCAGTATGAGAAAAGTGAAGTTCACCTCCCTATCAGTATGAGAAA 4399
DB 265 CTATCAGTATGAGAAAAGTGAAGTTCACCTCCCTATCAGTATGAGAAA 206
QY 4400 AGTGAAGTTCACCACTCCCTATCAGTATGAGAAAAGTGAAGTTCAGTTAC 4459
DB 205 AGTGAAGTTCACCACTCCCTATCAGTATGAGAAAAGTGAAGTTCAGTTAC 146
QY 4460 CACTCCCTATCAGTATGAGAAAAGTGAAGTTCACCTCCCTATCAGTATG 4519
DB 145 CACTCCCTATCAGTATGAGAAAAGTGAAGTTCACCTCCCTATCAGTATG 86
QY 4520 GAGAAAAGTGAAGTTCACCTCCCTATCAGTATGAGAAAAGTGAAGTTCAG 4579
DB 85 GAGAAAAGTGAAGTTCACCTCCCTATCAGTATGAGAAAAGTGAAGTTCAG 26
QY 4580 GCTCGTACCGAG 4591
DB 25 GCTCGTACCGAG 14

Search completed: August 30, 2005, 03:35:50
Job time : 655 secs

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XX The present sequence is that of MHCMintreO, an inducible, cardiac-
CC preferred promoter sequence derived from the mouse alpha-myosin heavy
CC chain promoter sequence. The native sequence was modified by insertion of
CC a 7-repeat Teco binding site sequence. The promoter comprises a responder
CC locus that is a copy number dependent, position independent locus in
CC which various transgenes can be inserted. When uninduced, these
CC transgenes are silent. When induced, the transgenes are very active.
CC These genes can then be turned off using the inducible system. The
CC promoter is useful for expressing operably linked sequences in a cardiac
CC tissue-preferred expression pattern. Expression cassettes, host cells and
CC transgenic animals are provided. The transgenic animals exhibit inducible
CC cardiac-preferred expression of a nucleotide sequence of interest, e.g.
CC BCL2 or glycogen synthase kinase 3-beta. These animals may have an
CC altered susceptibility to cardiopathology and may be useful for
CC identifying anti-cardiopathic compounds. The cardiopathology is
CC especially a cardiomyopathy such as familial hypertrophic
CC cardiomyopathies, dilated cardiomyopathies, peripartum cardiomyopathy,
CC restrictive cardiomyopathies, ischaemic heart disease, angina pectoris,
CC myocardial infarction, hypertensive heart disease and endocarditis
CC (claimed).

XX Sequence 5735 BP; 1458 A; 1455 C; 1545 G; 1277 T; 0 U; 0 Other;

Query Match 100.0%; Score 5735; DB 12; Length 5735;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGATCTCGCAAGTGCACAAAGGGTCTCCACCCACAGGTCCTTACTCAATTTAGT 60
DB 1 GGATCTCGCAAGTGCACAAAGGGTCTCCACCCACAGGTCCTTACTCAATTTAGT 60
QY 61 TTCATGCTTGTCTCAATGCTGGCTCCCGAGAGCTAATTTGACTTTGTTTAT 120
DB 61 TTCATGCTTGTCTCAATGCTGGCTCCCGAGAGCTAATTTGACTTTGTTTAT 120
QY 121 TTCAAAAGGGCTGAATGAGAGTAGATCTTGTCTACCCAGCTCTAAGGGTGGCTGA 180
DB 121 TTCAAAAGGGCTGAATGAGAGTAGATCTTGTCTACCCAGCTCTAAGGGTGGCTGA 180
QY 181 AGCCCTCAGACCTGAGCCTTTGCAACAGCCCTTTAGTGAAACAATAAAGCATTT 240
DB 181 AGCCCTCAGACCTGAGCCTTTGCAACAGCCCTTTAGTGAAACAATAAAGCATTT 240
QY 241 TCCTTAAAGCCAAATCTGCTCTAGACTCTTCTCTGACCTCGGTCCTGGCTCT 300
DB 241 TCCTTAAAGCCAAATCTGCTCTAGACTCTTCTCTGACCTCGGTCCTGGCTCT 300
QY 301 AGGCTGGGAGGTGGGCTTGAAGAAAGAGTGGGGAAGTGCAGAAAGCCGATCCTAG 360
DB 301 AGGCTGGGAGGTGGGCTTGAAGAAAGAGTGGGGAAGTGCAGAAAGCCGATCCTAG 360
QY 361 GGCCTGTGAAGTTCGAGGCTTCCCTGTACAGACTGGCTCATAGATCTCTCCAGCC 420
DB 361 GGCCTGTGAAGTTCGAGGCTTCCCTGTACAGACTGGCTCATAGATCTCTCCAGCC 420
QY 421 AAACATAGCAGAGTATCCTCTTGTGACTTCCACAGGCCAGTACTGTCAAGTT 480
DB 421 AAACATAGCAGAGTATCCTCTTGTGACTTCCACAGGCCAGTACTGTCAAGTT 480
QY 481 GAAACAGAGTTTAAAGAAAGCTTGAACCTCACTGAACCTGAAAGCTCATCACAAACA 540
DB 481 GAAACAGAGTTTAAAGAAAGCTTGAACCTCACTGAACCTGAAAGCTCATCACAAACA 540
QY 541 AGCAGCTAGGTCACCTGCTAGTTAGTATCTTAGCGATATATATGAGAGCTGGGCAC 600
DB 541 AGCAGCTAGGTCACCTGCTAGTTAGTATCTTAGCGATATATATGAGAGCTGGGCAC 600
QY 601 AGAAGTCTGGGGGTAGAGAACTGACAGTACTTTTCAGTCGGCAAAAGATATACCCCC 660
DB 601 AGAAGTCTGGGGGTAGAGAACTGACAGTACTTTTCAGTCGGCAAAAGATATACCCCC 660
QY 661 TCAGCAGATGTATATGTCCCTTAAATGCCATCCAGGAGGTCTTCTAAGAGACATG 720
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DB 661 TCAGCAGATGTATATGTCCCTTAAATGCCATCCAGGAGGTCTTAAAGAGACATG 720
QY 721 GGATGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 GGATGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 TTCACCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TTCACCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 GACACACCCCTGCTGAGAGATTTCAATTTCTTCTTCAAGTCCCTCTGTGACTTCAT 900
DB 841 GACACACCCCTGCTGAGAGATTTCAATTTCTTCTTCAAGTCCCTCTGTGACTTCAT 900
QY 901 TTGCAAGGCTTTGACCTGCGAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 TTGCAAGGCTTTGACCTGCGAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GCCATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 GCCATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 TCACTGCGCGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 TCACTGCGCGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 TACTCCCGAGATCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1081 TACTCCCGAGATCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1141 TGAAGACATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1141 TGAAGACATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 ACACTGTGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1201 ACACTGTGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 GCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1261 GCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1321 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 TGCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1381 TGCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 AGATTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 AGATTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 ATACCTCATCCCGTCTCCCAATTTAAAGCCACTTTCTTCTAGATCAGACTGAGCTGC 1560
DB 1501 ATACCTCATCCCGTCTCCCAATTTAAAGCCACTTTCTTCTAGATCAGACTGAGCTGC 1560
QY 1561 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1561 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 GCAACCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1621 GCAACCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1681 CTGTGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 CTGTGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 ATGGCGGGGGGGGGATTTTGGGGGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
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Db	1741	ATGGGCGGGGGGGGAGATTCTGGGGGGGGGAGAGAGAAAGTGAGAGAGAGGCTTGAAACAG	1800
Qy	1801	AGAAATCTGGAAAGCCCTGGAAACGATACCATTAAGGGAAAGAACCCAGGCTACCTTTAGATG	1860
Db	1801	AGAAATCTGGAAAGCCCTGGAAACGATACCATTAAGGGAAAGAACCCAGGCTACCTTTAGATG	1860
Qy	1861	TAAATCATGAAGAAGAGGAGAGAGGAAAGCTGGAGAGAGTGAAGAGACCCCGGGGCAAGA	1920
Db	1861	TAAATCATGAAGAAGAGGAGAGAGGAAAGCTGGAGAGAGTGAAGAGACCCCGGGGCAAGA	1920
Qy	1921	CATGGAAGCAAGGACAAGCCAGGTTGAGCGCTCCGTGAATCAACCTGCTGAAGGACAG	1980
Db	1921	CATGGAAGCAAGGACAAGCCAGGTTGAGCGCTCCGTGAATCAACCTGCTGAAGGACAG	1980
Qy	1981	CCCTGATATGAGACAACAAGCCAGGTTGAGCGCTCCGTGAATCAACCTGCTGAAGGACAG	2040
Db	1981	CCCTGATATGAGACAACAAGCCAGGTTGAGCGCTCCGTGAATCAACCTGCTGAAGGACAG	2040
Qy	2041	GTAGACACAGGAACAGACAGAGACGGGGGAGCCAGGTAAACAAGAAATGTCCTTCTCAC	2100
Db	2041	GTAGACACAGGAACAGACAGAGACGGGGGAGCCAGGTAAACAAGAAATGTCCTTCTCAC	2100
Qy	2101	CTTGAGCCAGAGCGTCCATCTGTGTCCACATACCTGTAAAGTTCAATCAGACTGACAGGC	2160
Db	2101	CTTGAGCCAGAGCGTCCATCTGTGTCCACATACCTGTAAAGTTCAATCAGACTGACAGGC	2160
Qy	2161	TGGCTTGGGAGGAGCTGGAAGAGATGTGAGAGCCAGGGGAGACAAGGGGGGCTTAGA	2220
Db	2161	TGGCTTGGGAGGAGCTGGAAGAGATGTGAGAGCCAGGGGAGACAAGGGGGGCTTAGA	2220
Qy	2221	AAGGAAGAAGGGGGCAAAACAAGCCACAACAAGGGGACAGACCCAGAACTGAGTTAACTC	2280
Db	2221	AAGGAAGAAGGGGGCAAAACAAGCCACAACAAGGGGACAGACCCAGAACTGAGTTAACTC	2280
Qy	2281	CTTCTTGTGTGATTTCTCCATAGAGAGGAGATGGGAACCTGTGTGACCAACATCCCCCATGA	2340
Db	2281	CTTCTTGTGTGATTTCTCCATAGAGAGGAGATGGGAACCTGTGTGACCAACATCCCCCATGA	2340
Qy	2341	GGCCCCATCACCCATACCAAGTTTGAGGCTGAGTGGAATTCTAGGTTCCCTGAGGACAGAG	2400
Db	2341	GGCCCCATCACCCATACCAAGTTTGAGGCTGAGTGGAATTCTAGGTTCCCTGAGGACAGAG	2400
Qy	2401	CCTGGCCCTTTGTCTTTGGAGCCTGACCCCAAGGTGACCCCAATGTTCTCAGTACCTTTGAA	2460
Db	2401	CCTGGCCCTTTGTCTTTGGAGCCTGACCCCAAGGTGACCCCAATGTTCTCAGTACCTTTGAA	2460
Qy	2461	GGCCTCAAGAGCTTGAAGAACCAAGGACAGTGAATATTAGGCAATGGGCTTAAACCTTGAGACT	2520
Db	2461	GGCCTCAAGAGCTTGAAGAACCAAGGACAGTGAATATTAGGCAATGGGCTTAAACCTTGAGACT	2520
Qy	2521	TGACACAGAGGCTCAAGGTGACCTCCAGGGGACAAGGTGACAGAGTGAGCCTTTATCC	2580
Db	2521	TGACACAGAGGCTCAAGGTGACCTCCAGGGGACAAGGTGACAGAGTGAGCCTTTATCC	2580
Qy	2581	CCAAAGACCAACCATTTTGSCATAGGTGGCTGCAATTGGAATGCAAGGTTGAATCAGGTC	2640
Db	2581	CCAAAGACCAACCATTTTGSCATAGGTGGCTGCAATTGGAATGCAAGGTTGAATCAGGTC	2640
Qy	2641	CCTTCAAGAAATACATGATGCAAGACCTTCAGGAGAGGGGATATGCTCTCTGCC	2700
Db	2641	CCTTCAAGAAATACATGATGCAAGACCTTCAGGAGAGGGGATATGCTCTCTGCC	2700
Qy	2701	CCACCCACATTAAGGGGAGTGAACCTATCCTAGGGGAGCTGGCGAACCCTTGGGAGACACAC	2760
Db	2701	CCACCCACATTAAGGGGAGTGAACCTATCCTAGGGGAGCTGGCGAACCCTTGGGAGACACAC	2760
Qy	2761	ATTACTGAGAGTGTGAGGCCCAAGAAAACCTGACCCGCTGTGTCTGTGCCACCTCCACAC	2820
Db	2761	ATTACTGAGAGTGTGAGGCCCAAGAAAACCTGACCCGCTGTGTCTGTGCCACCTCCACAC	2820
Qy	2821	TCTAAGCTTATTTAGAGGTGACAGTGAATAGGGTGGAGCTGGTAGCAGGGAGAGTGT	2880
Db	2821	TCTAAGCTTATTTAGAGGTGACAGTGAATAGGGTGGAGCTGGTAGCAGGGAGAGTGT	2880

QY	2881	TCTGGGTGTGAGGGGTGTAGGGGAAAAGCCAGACGAGGGGAGTCTGGCTTTGTCTCTCGAA	2940
Db	2881	TCTGGGTGTGAGGGGTGTAGGGGAAAAGCCAGACGAGGGGAGTCTGGCTTTGTCTCTCGAA	2940
QY	2941	CACAAATGCTACTTAGTTATACAGGATACCTGTCTAAAGACCACATCTACGACTTC	3000
Db	2941	CACAAATGCTACTTAGTTATACAGGATACCTGTCTAAAGACCACATCTACGACTTC	3000
QY	3001	TGAAAGAAGACAGACCCCTTGAGGACAGGGGTGTCTCTGAGCCTTGGGTCTTGATGTGT	3060
Db	3001	TGAAAGAAGACAGACCCCTTGAGGACAGGGGTGTCTCTGAGCCTTGGGTCTTGATGTGT	3060
QY	3061	CCAAAGAGGGGGATAGGTGTAGTTAAGGCCCCAGAGGCGTTATGAGAAAGGACCTTG	3120
Db	3061	CCAAAGAGGGGGATAGGTGTAGTTAAGGCCCCAGAGGCGTTATGAGAAAGGACCTTG	3120
QY	3121	GGAAGGGGTCAGTCTGACAGAGCCCTTATCCATGGAATCTTGGAGCTTGGGSCCACTGTGT	3180
Db	3121	GGAAGGGGTCAGTCTGACAGAGCCCTTATCCATGGAATCTTGGAGCTTGGGSCCACTGTGT	3180
QY	3181	TAAATCTCTGGGGCTGGCAGGCAATTCAAAGCAGACTTGCATCCTCTGGAGCCTGGGG	3240
Db	3181	TAAATCTCTGGGGCTGGCAGGCAATTCAAAGCAGACTTGCATCCTCTGGAGCCTGGGG	3240
QY	3241	GGCGGAAGGGAGAGCAACCCCCCACTTATACCTTTCTCCCTCAGGCCCCAGGATTTAACCT	3300
Db	3241	GGCGGAAGGGAGAGCAACCCCCCACTTATACCTTTCTCCCTCAGGCCCCAGGATTTAACCT	3300
QY	3301	CTGGCCTTCCCTTCCCACTCCCATCAGAGGTGAGGGGTTGCAGAGGGAGGTTAAAA	3360
Db	3301	CTGGCCTTCCCTTCCCACTCCCATCAGAGGTGAGGGGTTGCAGAGGGAGGTTAAAA	3360
QY	3361	CCTACATGTCCAAACATCATCATGTGTGACAGATATATGATACGTATGTGTAGAGGCAAAA	3420
Db	3361	CCTACATGTCCAAACATCATCATGTGTGACAGATATATGATACGTATGTGTAGAGGCAAAA	3420
QY	3421	GGAATCTGACAGGCTTAACTGGGGTTAAATGTGTAAAGTCTGTGTGCATGTGTGTGTCTG	3480
Db	3421	GGAATCTGACAGGCTTAACTGGGGTTAAATGTGTAAAGTCTGTGTGCATGTGTGTGTCTG	3480
QY	3481	ACTGAAAAAGGGGATGGCTGTGTGACGCTGTTCACTTCTGTGTGTGAGGTTACCAACTGCA	3540
Db	3481	ACTGAAAAAGGGGATGGCTGTGTGACGCTGTTCACTTCTGTGTGTGAGGTTACCAACTGCA	3540
QY	3541	GGTTTGTGTAAATTTGGCCCAAGGCAAGTGGGTGAATCCCTTCATGCTTTTAAAGAT	3600
Db	3541	GGTTTGTGTAAATTTGGCCCAAGGCAAGTGGGTGAATCCCTTCATGCTTTTAAAGAT	3600
QY	3601	TGATGTATGGCCTGCATCTCAAGGACCAATGAAAAATGAATGACACTCTATATGTGTCT	3660
Db	3601	TGATGTATGGCCTGCATCTCAAGGACCAATGAAAAATGAATGACACTCTATATGTGTCT	3660
QY	3661	CTAAGCTTAAGTACCAAGGCTTTTGGAGGACACCTGTCTTGAAGATGTGGGCAACAGAGAC	3720
Db	3661	CTAAGCTTAAGTACCAAGGCTTTTGGAGGACACCTGTCTTGAAGATGTGGGCAACAGAGAC	3720
QY	3721	TACAGACAGTATCTGTACAGAGTAAAGAGAGAGAGAGGGGGTGTAGAAATTTCTTTCTA	3780
Db	3721	TACAGACAGTATCTGTACAGAGTAAAGAGAGAGAGAGGGGGTGTAGAAATTTCTTTCTA	3780
QY	3781	TCAAAGGGAACCTGAGTGTGTGACCTTGCAAGTGAATGTCTTCCCTTGAACAATCACTGACTT	3840
Db	3781	TCAAAGGGAACCTGAGTGTGTGACCTTGCAAGTGAATGTCTTCCCTTGAACAATCACTGACTT	3840
QY	3841	TGTCTCTGGGAGCAGACTGTGGAACCTTCAAGGCTTGAAGAGTAAAGAGGCTCCCTCA	3900
Db	3841	TGTCTCTGGGAGCAGACTGTGGAACCTTCAAGGCTTGAAGAGTAAAGAGGCTCCCTCA	3900
QY	3901	GCTGAACCTATGCAGATATGCAAGGCTTGAAGAGGGGGAAGGAGAGCCTTGGGATGGAGC	3960
Db	3901	GCTGAACCTATGCAGATATGCAAGGCTTGAAGAGGGGGAAGGAGAGCCTTGGGATGGAGC	3960

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Qy 3961 TTGTGTTGGAGGACAGGGGACAGATATTAAGCCTGGAGAGAGAGTGAACCTTTACCCAG 4020
Db 3961 TTGTGTTGGAGGACAGGGGACAGATATTAAGCCTGGAGAGAGAGTGAACCTTTACCCAG 4020
Qy 4021 TTGTTCACATCAACCTTCAGATTAAATACTGAGGTAAAGGCTGGTAAAGGGAGGTG 4080
Db 4021 TTGTTCACATCAACCTTCAGATTAAATACTGAGGTAAAGGCTGGTAAAGGGAGGTG 4080
Qy 4081 GTGTGAGACGCTCTGTCTCTCTCTGATGACCTGAGGCGCTTTGGGAGAGAGAAATGT 4140
Db 4081 GTGTGAGACGCTCTGTCTCTCTCTGATGACCTGAGGCGCTTTGGGAGAGAGAAATGT 4140
Qy 4141 GCGCAAGACTAAAAAAGGCGCATGAGCCAGAGGGGCGAGGGACAGACCTTTCAATGG 4200
Db 4141 GCGCAAGACTAAAAAAGGCGCATGAGCCAGAGGGGCGAGGGCAACAGACCTTTCAATGG 4200
Qy 4201 GCAAACTTGGGGGCGGTAGTATGATGACAAAGAACTGGCCAAATGATACCTTTCTTC 4260
Db 4201 GCAAACTTGGGGGCGGTAGTATGATGACAAAGAACTGGCCAAATGATACCTTTCTTC 4260
Qy 4261 TTCTAAGGACAGGAGGAACTCGAGTTTACACTCCCTATCAGTATAGAGAAAGTGA 4320
Db 4261 TTCTAAGGACAGGAGGAACTCGAGTTTACACTCCCTATCAGTATAGAGAAAGTGA 4320
Qy 4321 AAGTCAGATTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTC 4380
Db 4321 AAGTCAGATTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTC 4380
Qy 4381 CCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAA 4440
Db 4381 CCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAA 4440
Qy 4441 AAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTAC 4500
Db 4441 AAGTGAAGTGAAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTAC 4500
Qy 4501 CCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTAT 4560
Db 4501 CCACTCCCTATCAGTATAGAGAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTAT 4560
Qy 4561 AGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4620
Db 4561 AGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4620
Qy 4621 TATGGAATGGGATATTAAGGGGCTGAGACTGAGAGCTGAGAGATTTCTCCACCA 4680
Db 4621 TATGGAATGGGATATTAAGGGGCTGAGACTGAGAGCTGAGAGATTTCTCCACCA 4680
Qy 4681 GGTAAAGAGGATTTGGGCTGGGGCTCTTCAACCAACCAACCTCTCCACCTAGAA 4740
Db 4681 GGTAAAGAGGATTTGGGCTGGGGCTCTTCAACCAACCAACCTCTCCACCTAGAA 4740
Qy 4741 GGAACCTGCTTCTGGAAGTGGGGTTCAGGCGGCTCAGAGATCTAAGGGGGCTT 4800
Db 4741 GGAACCTGCTTCTGGAAGTGGGGTTCAGGCGGCTCAGAGATCTAAGGGGGCTT 4800
Qy 4801 CCACCAAGCTGGGAAGTTCTCAGTGGGAGAGGTTTCCACAAAGAAACATGAGGCCCT 4860
Db 4801 CCACCAAGCTGGGAAGTTCTCAGTGGGAGAGGTTTCCACAAAGAAACATGAGGCCCT 4860
Qy 4861 TCCCTTAAGCTGCTTCTCCATCTCTCTGAGGATGCTCTCTCCCGTCTTGTTATC 4920
Db 4861 TCCCTTAAGCTGCTTCTCCATCTCTCTGAGGATGCTCTCTCCCGTCTTGTTATC 4920
Qy 4921 TTGGCTCTGCTCTTTCAGCAAGATTTGGCGCTGCTGCTCACTTCTCTACTGT 4980
Db 4921 TTGGCTCTGCTCTTTCAGCAAGATTTGGCGCTGCTGCTCACTTCTCTACTGT 4980
Qy 4981 CTCGCTGCTTGCCTTGCCTTCTTGCGTGTCTTCTTCCACCATTTCTCACTTACC 5040
Db 4981 CTCGCTGCTTGCCTTGCCTTCTTGCGTGTCTTCTTCCACCATTTCTCACTTACC 5040
Qy 5041 TTTTCTCCCTTCTCATTTGATTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5100

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Db 5041 TTTTCTCCCTTCTCATTTGATTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5100
Qy 5101 CTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5160
Db 5101 CTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5160
Qy 5161 CTGTGTCAAGATGCTGAGATCAACACTGGGGTTCACACCTTATATTAACAATCTTCA 5220
Db 5161 CTGTGTCAAGATGCTGAGATCAACACTGGGGTTCACACCTTATATTAACAATCTTCA 5220
Qy 5221 GTGAGCCACAGCTTCAGTGTCTGGGTGCTCTTACCTTCTCAACCCCTGGCTTGTG 5280
Db 5221 GTGAGCCACAGCTTCAGTGTCTGGGTGCTCTTACCTTCTCAACCCCTGGCTTGTG 5280
Qy 5281 CTGTTCATCTGCTGCTGAGATCTCTGATTTGTGCTCCAGCCCTGTCTCTCTTCTCT 5340
Db 5281 CTGTTCATCTGCTGCTGAGATCTCTGATTTGTGCTCCAGCCCTGTCTCTCTTCTCT 5340
Qy 5341 GCGTGTCTCTCTCTCTGTCAGCTGGCCACTGTGGTGTCTGCTCAAGCTGTGTCTCA 5400
Db 5341 GCGTGTCTCTCTCTCTGTCAGCTGGCCACTGTGGTGTCTGCTCAAGCTGTGTCTCA 5400
Qy 5401 ATTCTTCAAGATTTCTGAAAAGTTAACAGAGTGAATGTTTCCCTGTGACAGACAG 5460
Db 5401 ATTCTTCAAGATTTCTGAAAAGTTAACAGAGTGAATGTTTCCCTGTGACAGACAG 5460
Qy 5461 TCAAGATTTCTCCCGGAGGCTCAAGGCTTCAAGCCCTCTTCTGTCGCAAGCTCCGGCA 5520
Db 5461 TCAAGATTTCTCCCGGAGGCTCAAGGCTTCAAGCCCTCTTCTGTCGCAAGCTCCGGCA 5520
Qy 5521 CTCTTGAACAACTCTCAGGACCTTACCCCACTAGACCTCTGACAGAGAGAGGACCT 5580
Db 5521 CTCTTGAACAACTCTCAGGACCTTACCCCACTAGACCTCTGACAGAGAGAGGACCT 5580
Qy 5581 TTTCATGAGTCTCTGTGGAGAGCCATAGGCTTACGCTGTAAAGAGGACAGGAAATGTGT 5640
Db 5581 TTTCATGAGTCTCTGTGGAGAGCCATAGGCTTACGCTGTGTAAAGAGGACAGGAAATGTGT 5640
Qy 5641 GGTGTAGGAAAGTCAAGACTTCAATAGAAAGCTTACCCCAACCCAGAAATGACAGACAG 5700
Db 5641 GGTGTAGGAAAGTCAAGACTTCAATAGAAAGCTTACCCCAACCCAGAAATGACAGACAG 5700
Qy 5701 TCCCTCTATCTTCCCATTAAGATTTGAGTGCAC 5735
Db 5701 TCCCTCTATCTTCCCATTAAGATTTGAGTGCAC 5735

RESULT 2
AAD02408
ID AAD02408 standard; DNA; 5443 BP.
XX
AC AAD02408;
XX
DT 24-APR-2001 (first entry)
XX
XX
XX Mouse alpha-cardiac myosin heavy chain (MHC) promoter.
XX
XX Mouse; cyclin D2; CYCD2; cardiomyocyte cell; screening; therapy;
XX infarct; cardiomyocyte cell proliferation enhancer; gene therapy;
XX infarct; cardiomyopathy; alpha-cardiac myosin heavy chain; MHC; ds.
XX Mus musculus.
XX
XX MO200078119-A2.
XX
XX 28-DEC-2000.
XX
XX 19-JUN-2000; 2000MO-US016827.
XX
XX 18-JUN-1999; 99US-0139942P.
XX
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
PA

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XX Field ID, Pasumarchi KBS;
XX WPI; 2001-102575/11.

PT Increasing proliferative potential of cardiomyocyte cell which is used
PT for screening activity of biological or pharmacological agent, involves
PT increasing the level of cyclin D2 activity in cardiomyocyte cell.

XX Example 1; Page 62-66; 67bp; English.

XX The present sequence is mouse alpha-cardiac myosin heavy chain (MHC)
CC promoter. This sequence is used in the preparation of a MHC-CYCD2 fusion
CC gene. The cyclin D2 (CYCD2) cDNA sequence is used to increase the
CC proliferative potential of a cardiomyocyte cell by increasing the level
CC of cyclin D2 activity in the cardiomyocyte cell. The transgenic animals
CC expressing cyclin D2 have sustained atrial and ventricular cardiomyocyte
CC DNA synthesis. Cardiomyocyte cells with enhanced proliferative potential
CC are useful for screening the activity of biological or pharmacological
CC agents on cardiomyocyte cells. Genetically modified cardiomyocyte cells
CC are useful for delivering therapeutics to mammals. The cells are also
CC useful to target an improvement of the contractile function of the heart
CC of the patient, for e.g. in the treatment of contractile losses due to
CC infarcts or cardiomyopathies

XX Sequence 5443 BP; 1352 A; 1399 C; 1492 G; 1200 T; 0 U; 0 Other;

Query Match 88.0%; Score 5045; DB 5; Length 5443;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 5383; Conservative 0; Mismatches 60; Indels 292; Gaps 1;

QY 1 GGATTCCTGCAAGGTCACAAAGGCTCCACCCACGAGTCCCTGTCATTTCACT 60
DB 1 GGATTCCTGCAAGGTCACAAAGGCTCCACCCACGAGTCCCTGTCATTTCACT 60
QY 61 TTCATGCTTGTCTCACAATGCTGGCTCCACAGCTTAATTTGACTTTTAT 120
DB 61 TTCATGCTTGTCTCACAATGCTGGCTCCACAGCTTAATTTGACTTTTAT 120
QY 121 TTCAAAAGGCTGATGAGAGATGATCTTTGCTACCAAGCTTAAGGTCGCTGA 180
DB 121 TTCAAAAGGCTGATGAGAGATGATCTTTGCTACCAAGCTTAAGGTCGCTGA 180
QY 181 AGGCTCAGACCTGAGACCTTTGCAAGCCCTTAGTGGAAGCAATTAAGCAATT 240
DB 181 AGGCTCAGACCTGAGACCTTTGCAAGCCCTTAGTGGAAGCAATTAAGCAATT 240
QY 241 TCCTTAAGCCAAATCTGCTCTAGACTCTTCTCTGACTCGGTCCTGAGCTCT 300
DB 241 TCCTTAAGCCAAATCTGCTCTAGACTCTTCTCTGACTCGGTCCTGAGCTCT 300
QY 301 AGGCTGGAAGTGGGCTTGAAGAAAGATGGGGAAGTGGCAAAAGCCGATCCCTAG 360
DB 301 AGGCTGGAAGTGGGCTTGAAGAAAGATGGGGAAGTGGCAAAAGCCGATCCCTAG 360
QY 361 GGCCCTGTGAAGTTCGAGGCTTCCCTGTAAGAGATGAGTCTCTCTCCAGCC 420
DB 361 GGCCCTGTGAAGTTCGAGGCTTCCCTGTAAGAGATGAGTCTCTCTCCAGCC 420
QY 421 AAACATGACAGAGATGATCTCTTGTGACTTCCCAAGGCGCCAGTACTGTGAGTT 480
DB 421 AAACATGACAGAGATGATCTCTTGTGACTTCCCAAGGCGCCAGTACTGTGAGTT 480
QY 481 GAAACAGAGATTTAGAGAGCTCTGAAGCTCACTGAAGCTCATCCAAAGCA 540
DB 481 GAAACAGAGATTTAGAGAGCTCTGAAGCTCACTGAAGCTCATCCAAAGCA 540
QY 541 AGCAGCTTAGGTGCACTGCTAGTATCTCTAGCTGATTAATTTGAGAGCTGGGCGAC 600
DB 541 AGCAGCTTAGGTGCACTGCTAGTATCTCTAGCTGATTAATTTGAGAGCTGGGCGAC 600
QY 601 AGAAGTCTGTGGGTGTAGAACTGACAGTGAATTTCACTGGCAAGGATATGACCCCG 660
DB 601 AGAAGTCTGTGGGTGTAGAACTGACAGTGAATTTCACTGGCAAGGATATGACCCCG 660

DB 601 AGAAGTCTGTGGGTGTAGAACTGACAGTGAATTTCACTGGCAAGGATATGACCCCG 660
QY 661 TCAGCAGATGTAGTATGCTCCCTAGATCCCATCCAGGCAAGTCTCTAAGAGCATG 720
DB 661 TCAGCAGATGTAGTATGCTCCCTAGATCCCATCCAGGCAAGTCTCTAAGAGCATG 720
QY 721 GGATGAGAGATGTACTCATGTGAGCTCAATCCAAACAGCATTCACAGTGTCCCTGGCCC 780
DB 721 GGATGAGAGATGTACTCATGTGAGCTCAATCCAAACAGCATTCACAGTGTCCCTGGCCC 780
QY 781 TTCACCTTAGCCAGAGAGACATTAACCTTAGCCTATCTTCTCTCCCATCCCTCCAG 840
DB 781 TTCACCTTAGCCAGAGAGACATTAACCTTAGCCTATCTTCTCTCCCATCCCTCCAG 840
QY 841 GACACACCCCTGCTGAGTATCTTCTCTTCAAGCTCCCTCTGAGCTTCCAT 900
DB 841 GACACACCCCTGCTGAGTATCTTCTCTTCAAGCTCCCTCTGAGCTTCCAT 900
QY 901 TTGCAAGGCTTTTGAATCTGCAAGCTGCTGGAAGATGATTTGAGCTGAGTGGCA 960
DB 901 TTGCAAGGCTTTTGAATCTGCAAGCTGCTGGAAGATGATTTGAGCTGAGTGGCA 960
QY 961 GCCATCTCAAGAGAAAGACACACAGAGGAGCCAGATTTTGAAGATCAGAACTAA 1020
DB 961 GCCATCTCAAGAGAAAGACACACAGAGGAGCCAGATTTTGAAGATCAGAACTAA 1020
QY 1021 TCACCTGGGCGGCTGGGTGAGAAAGAGTGAATGCTCCGCTCAAGTAAAGCAAGC 1080
DB 1021 TCACCTGGGCGGCTGGGTGAGAAAGAGTGAATGCTCCGCTCAAGTAAAGCAAGC 1080
QY 1081 TAGTCCCGGAGATCTGCTCCACAGCTGGGCTGCTGGGATGCTTTAGAAATGGGCTC 1140
DB 1081 TAGTCCCGGAGATCTGCTCCACAGCTGGGCTGCTGGGATGCTTTAGAAATGGGCTC 1140
QY 1141 TGAAGAACAATGGATTTGGAAGACATCTCTTTGAGTCTTCCCTCAACCCCACTACAGAC 1200
DB 1141 TGAAGAACAATGGATTTGGAAGACATCTCTTTGAGTCTTCCCTCAACCCCACTACAGAC 1200
QY 1201 AACCTGTGTGTGGCAGACTCTGTCAACAGCCCTGTGTGACCACTGAGCTAG 1260
DB 1201 AACCTGTGTGTGGCAGACTCTGTCAACAGCCCTGTGTGACCACTGAGCTAG 1260
QY 1261 GCAACAGAGCATGTGGGCTGTGCTGAGATGAAGATGTTGTTACCAATGCAAAACAG 1320
DB 1261 GCAACAGAGCATGTGGGCTGTGCTGAGATGAAGATGTTGTTACCAATGCAAAACAG 1320
QY 1321 CAGGGAGGAGGACACAGAAAGAAATTAAGAGAGAGAGAAAGCCGATCAATCAGA 1380
DB 1321 CAGGGAGGAGGACACAGAAAGAAATTAAGAGAGAGAGAAAGCCGATCAATCAGA 1380
QY 1381 TGCAGTCAGAGAGATGGGAAGCCACACAGCTTTGAGCAGAGAGAAACAGAAAGGGAG 1440
DB 1381 TGCAGTCAGAGAGATGGGAAGCCACACAGCTTTGAGCAGAGAGAAACAGAAAGGGAG 1440
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DB 1441 AGATTCGTGGGCAATAAGAGGAGCCAGAAAGAGAGCCAGGCCCCCAAGTCTCCCTTT 1500
QY 1501 ATACCTCATCCCGTCTCCCAATTAAGCCACTTCTCTCTAGATCAGACTGAGCTGC 1560
DB 1501 ATACCTCATCCCGTCTCCCAATTAAGCCACTTCTCTCTAGATCAGACTGAGCTGC 1560
QY 1561 AGCGAAGAGACCCGTAAGGAGATCACTGATGAAGAGATGTGTGAGAGAGTCCAGG 1620
DB 1561 AGCGAAGAGACCCGTAAGGAGATCACTGATGAAGAGATGTGTGAGAGAGTCCAGG 1620
QY 1621 GGAACCTTAAGAGCCAGGCTTAAGAGCAAGATTAAGGAGCTTCAAGAGTGGCAGG 1680
DB 1621 GGAACCTTAAGAGCCAGGCTTAAGAGCAAGATTAAGGAGCTTCAAGAGTGGCAGG 1680
QY 1681 CTGTGACACAGAGGCTGAGAGCTGTGTGAGAGCTTCAAGATTAAGATGAATGCTCAGA 1740
DB 1681 CTGTGACACAGAGGCTGAGAGCTGTGTGAGAGCTTCAAGATTAAGATGAATGCTCAGA 1740

Qy 1741 ATGGGCGGGGGGGGATTTCTGGGGGGGGAGAGAGAGGTGAGAAAGGACCTTGAAACAG 1800
Db 1741 ATGGGCGGGGGGGGAGTTCTGGGGGGGGGAGAGAGAGGTGAGAAAGGACCTTGAAACAG 1800
Qy 1801 AGAATCTGGAGGCGTGGAAAACGATACCATTAAGGAGAAACCCAGGCTTACCTTTAGATG 1860
Db 1801 AGAATCTGGAGGCGTGGAAAACGATACCATTAAGGAGAAACCCAGGCTTACCTTTAGATG 1860
Qy 1861 TAAATCATGAAAAGCAGGAGAGAGGAGGAGCTGGAGAGGTAGAGAGAGCCCGGGGGCAAGA 1920
Db 1861 TAAATCATGAAAAGCAGGAGAGAGGAGGAGGAGCTGGAGAGGTAGAGAGAGCCCGGGGGCAAGA 1920
Qy 1921 CATGGAAGCAAGGACAAAGCCAGGTTGAGCGCTCCGTGAAAATCAAGCTCTGTAAGGCAAG 1980
Db 1921 CATGGAAGCAAGGACAAAGCCAGGTTGAGCGCTCCGTGAAAATCAAGCTCTGTAAGGCAAG 1980
Qy 1981 CCTGTGATAGACCCAGAAACAGAGGCTAGGGTTAATGTGAGACAGGAAACAGAG 2040
Db 1981 CCTGTGATAGACCCAGAAACAGAGGCTAGGGTTAATGTGAGACAGGAAACAGAG 2040
Qy 2041 GTAGACACAGGAACAGACAGAGAGGGGGGACAGGTAACAAGAGATGGTCCCTTCAC 2100
Db 2041 GTAGACACAGGAACAGACAGAGAGGGGGGACAGGTAACAAGAGATGGTCCCTTCAC 2100
Qy 2101 CTGTGGCAGAGCGTCCATCTGTGTCCACATACTCTAGAAATGTTTCATCAGACTGCAAGG 2160
Db 2101 CTGTGGCAGAGCGTCCATCTGTGTCCACATACTCTAGAAATGTTTCATCAGACTGCAAGG 2160
Qy 2161 TGGCTTGGAGGAGCTGTAAGAGATATGTGAGAGCCAGGGGAGACAAAGGGGCTTAGGA 2220
Db 2161 TGGCTTGGAGGAGCTGTAAGAGATATGTGAGAGCCAGGGGAGACAAAGGGGCTTAGGA 2220
Qy 2221 AAGGAAGAGGGGCAAAACAGGCGCACACAAGAGGGAGAGCCAGAACTGAGTTAACTC 2280
Db 2221 AAGGAAGAGGGGCAAAACAGGCGCACACAAGAGGGAGAGCCAGAACTGAGTTAACTC 2280
Qy 2281 CTTCCTTGTTCATCTTCATAGAGGAGAGTGGGAACTGTGACCACTATCCCATGA 2340
Db 2281 CTTCCTTGTTCATCTTCATAGAGGAGAGTGGGAACTGTGACCACTATCCCATGA 2340
Qy 2341 GCGCCCACTACCCATACCAAGTTGGCTGAGTGGCAATCTAGGTTCCCTGAGAGCAG 2400
Db 2341 GCGCCCACTACCCATACCAAGTTGGCTGAGTGGCAATCTAGGTTCCCTGAGAGCAG 2400
Qy 2401 CCTGGCCTTGTCTCTTGAGACCTGACCAAGCTGACCAATGTTCTCAGATACCTTGAAT 2460
Db 2401 CCTGGCCTTGTCTCTTGAGACCTGACCAAGCTGACCAATGTTCTCAGATACCTTGAAT 2460
Qy 2461 GCGCTCAAGAGCTTGAGAACAGGAGCTGACATATTAGGCTATGAGCTTAACTGAGCT 2520
Db 2461 GCGCTCAAGAGCTTGAGAACAGGAGCTGACATATTAGGCTATGAGCTTAACTGAGCT 2520
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Db 2521 TGACACAGAGGCTTCAAGTGAACCTCAAGGAGCAGCTGACAGCAGAGTGGCTTTATCC 2580
Qy 2581 TGCACACAGAGGCTTCAAGTGAACCTCAAGGAGCAGCTGACAGCAGAGTGGCTTTATCC 2640
Db 2581 TGCACACAGAGGCTTCAAGTGAACCTCAAGGAGCAGCTGACAGCAGAGTGGCTTTATCC 2640
Qy 2641 CTTTCAAGAAATATGCAATGCAATGAGAGCTTAAAGAGAGAGAGGAGTATGCTCTGCC 2700
Db 2641 CTTTCAAGAAATATGCAATGCAATGAGAGCTTAAAGAGAGAGAGGAGTATGCTCTGCC 2700
Qy 2701 CCACCCACATTAAGGGAGTGAATCTATCTGAGGGGCTGGGACCTTTGGGGAGACACAC 2760
Db 2701 CCACCCACATTAAGGGAGTGAATCTATCTGAGGGGCTGGGACCTTTGGGGAGACACAC 2760
Qy 2761 ATTACTGAGAGTGTGAGAGCCAGAAAAATGACCGGCTGTGTCTGCTCCACTTCCAC 2820
Db 2761 ATTACTGAGAGTGTGAGAGCCAGAAAAATGACCGGCTGTGTCTGCTCCACTTCCAC 2820

Qy 2821 TCTAGAGCTATAATGAGAGTGAACAGTATAGAGTGGAGGCTGTAGACAGGAGAGTGT 2880
Db 2821 TCTAGAGCTATAATGAGAGTGAACAGTATAGAGTGGAGGCTGTAGACAGGAGAGTGT 2880
Qy 2881 TCCGTGGTGTGAGGCTGTAGGGGAAAGCCAGAGCAGGGGAGTGTGGCTTTGTCTCTGAA 2940
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Db 2941 CACAATGTCTACTAGTATTAACAGGATGACCTGTAAAGACCCAACTTACGACCTC 3000
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Db 3121 GGAAGGGGTCAAGTCTGAGAGCCCTATCATGGAATCTGAGCCTGGGGCCAACTGTG 3180
Qy 3181 TAAATCTGTGGCTGAGAGGATTCGAAAGCAGACCTGCAATCTGTGCAAGCTGGGGA 3240
Db 3181 TAAATCTGTGGCTGAGAGGATTCGAAAGCAGACCTGCAATCTGTGCAAGCTGGGGA 3240
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Db 3481 ACTGAAAGAGGGGATGGCTGTGACGCTGTTCAGTTCTGTGCGTGAAGTTAACGAGCTGCA 3540
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Db 3661 CTAAAGCTAAGGTAGCAAGGCTTTGAGAGACACTGTCTAGAGATGTGGCAACAGAGAC 3720
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Db 3721 TACAGACAGTATCTGTACAGAGTAAGAGAGAGAGAGGGGGGTGTAATTTCTTTACTA 3780
Qy 3781 TCAAGAGGAACTGAATGTGTGCACTGTGCAAGAGTGAATGCTCTCCCTAGACATGAGCTT 3840
Db 3781 TCAAGAGGAACTGAATGTGTGCACTGTGCAAGAGTGAATGCTCTCCCTAGACATGAGCTT 3840
Qy 3841 TGTCTGTGGGAGCCAGCACTGTGGAATCTAGAGTCTGAGAGATGAGAGGCTCCCTCA 3900
Db 3841 TGTCTGTGGGAGCCAGCACTGTGGAATCTAGAGTCTGAGAGATGAGAGGCTCCCTCA 3900
Qy 3901 GCCTGAAGCTATGACAGATAGCCAGGGTTGAAAGGGGGAAGGAGAGCCTGGGATGGAGC 3960


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Db 3901 GCCTGAAGCATATGCAAGTATGCAAGGGTGAAGGGGGAAGGAGAGCTTGGAATGGGAGC 3960
Qy 3961 TTGTGTTGGAGGACAGGGGACAGATTTAAAGCTTGAGAGAAAGGTGACCTTACCCAG 4020
Db 3961 TTGTGTTGGAGGACAGGGGACAGATTTAAAGCTTGAGAGAAAGGTGACCTTACCCAG 4020
Qy 4021 TTGTGAACCTCAGCTTCAGATTTAAATAATGAGAGTAAGGGGCTGGGTAGGGGAGGTG 4080
Db 4021 TTGTGAACCTCAGCTTCAGATTTAAATAATGAGAGTAAGGGGCTGGGTAGGGGAGGTG 4080
Qy 4081 GTGTGAGACGCTCTGTCTCTCTCTGATGCTGAGGCTGAGGCTTTTGGGAGAGAGATGT 4140
Db 4081 GTGTGAGACGCTCTGTCTCTCTCTGATGCTGAGGCTGAGGCTTTTGGGAGAGAGATGT 4140
Qy 4141 GCCCAAGACTAAAAAAGGCGATGAGAGCGAGGGGCGAGGCAACAGCTTTTCATGG 4200
Db 4141 GCCCAAGACTAAAAAAGGCGATGAGAGCGAGGGGCGAGGCAACAGCTTTTCATGG 4200
Qy 4201 GCAACCTTGGGGGCGGTAGTATGATGATGACAAGAACTGCGCAATCGATACCTTCTTC 4260
Db 4201 GCAACCTTGGGGGCGGTAGTATGATGATGACAAGAACTGCGCAATCGATACCTTCTTC 4260
Qy 4261 TTCTTAAAGGACAGAGAGGAACTGAGATTTCACCTCCTATCAGTATAGAGAAAGTGA 4320
Db 4261 GGAGCCAGGACAGAGAGGAAAGTGGAGGAG----- 4291
Qy 4321 AAGTCGATTTCACCTCCTATCAGTATAGAGAAAGTGAAGTTCAGATTACCACTC 4380
Db 4321 ----- 4291
Qy 4381 CCTATCAGTATAGAGAAAGTGAAGTTCAGATTTCACCTCCTATCAGTATAGAGAA 4440
Db 4381 ----- 4291
Qy 4441 AAGTGAAGTCGAGTTTACCACTCCTATCAGTATAGAGAAAGTGAAGTTCAGATTTC 4500
Db 4441 ----- 4291
Qy 4501 CCACTCCTATCAGTATAGAGAAAGTGAAGTTCAGATTTCACCTCCTATCAGTAT 4560
Db 4501 ----- 4291
Qy 4561 AAGAGAAAGTGAAGTTCAGAGCTGCTACCGACAGAGACTCCAAATTTAGGCGAGGCA 4620
Db 4561 ----- 4291
Qy 4621 TATGGATGGGATATTAAGGGGCTGAGAGCTGAGAGCTGTCAGAGATTTCACCAACCA 4680
Db 4621 TATGGATGGGATATTAAGGGGCTGAGAGCTGAGAGCTGTCAGAGATTTCACCAACCA 4680
Qy 4681 GGTAAAGGAGTTCGGGAGTGGGGCTTCACCAACCAACCACTCTCCCACTAGAA 4740
Db 4681 GGTAAAGGAGTTCGGGAGTGGGGCTTCACCAACCAACCACTCTCCCACTAGAA 4740
Qy 4741 GGAACCTGCTTCCTGAGAGTGGGGTCAAGGCGGCTGAGAGTTCGACAGGGTGGCTT 4800
Db 4741 GGAACCTGCTTCCTGAGAGTGGGGTCAAGGCGGCTGAGAGTTCGACAGGGTGGCTT 4800
Qy 4801 CCAACGCTGGAGAGTTCAGTGGGAGAGGTTTCACCAAAACCACTGATGACCCCT 4860
Db 4801 CCAACGCTGGAGAGTTCAGTGGGAGAGGTTTCACCAAAACCACTGATGACCCCT 4860
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Db 4861 TCCCTTAAGCTGCTTCATCTCTCTCTGAGAGTCTCTCTCCGCTGTTGATTATC 4920
Qy 4921 TTGGCTCTGCTTGAAGAGATTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4980
Db 4921 TTGGCTCTGCTTGAAGAGATTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4980
Qy 4981 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040

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Db 4689 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4748
Qy 5041 TTTTCTCCCTCTCTCATTTGATTTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5100
Db 4749 TTTTCTCCCTCTCTCATTTGATTTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4808
Qy 5101 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5160
Db 4809 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4868
Qy 5161 CTGTGTCAGAGTCTGAGATTCACACCTGGGGTTCACACCTTATGTAACAATCTTCCA 5220
Db 4869 CTGTGTCAGAGTCTGAGATTCACACCTGGGGTTCACACCTTATGTAACAATCTTCCA 4928
Qy 5221 GTGAGCCACAGCTTCAAGTCTGCTGGGTCTCTTACCTTCTCAACCCCTGCTGCTGCT 5280
Db 4929 GTGAGCCACAGCTTCAAGTCTGCTGGGTCTCTTACCTTCTCAACCCCTGCTGCTGCT 4988
Qy 5281 CTGTTCACATCCCTGATCAGAGTCTAGATGATGCTCCAGAGCTGCTGCTGCTGCTGCT 5340
Db 4989 CTGTTCACATCCCTGATCAGAGTCTAGATGATGCTCCAGAGCTGCTGCTGCTGCTGCT 5048
Qy 5341 GCTGTCTCTCTCTGTGTCAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTG 5400
Db 5049 GCTGTCTCTCTCTGTGTCAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTG 5108
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Db 5109 ATTCTTCAAGATTTCTGAAAAAGTTAACAGAGTGAAGTATTCCTGTATACAGACAGA 5168
Qy 5461 TCACGATCTCCCGAAGTCAAGGCTTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5520
Db 5169 TCACGATCTCCCGAAGTCAAGGCTTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5228
Qy 5521 CTCTTACGAAACCTCAGGACCTTACCCACATAGACCTTGAAGAGAGAGAGAGAGAGACT 5580
Db 5229 CTCTTACGAAACCTCAGGACCTTACCCACATAGACCTTGAAGAGAGAGAGAGAGACT 5288
Qy 5581 TTACATGAGTCTGTGTGGAGAGAGCCATAGGCTTACGCTGTTAAAGAGAGAGAGAGT 5640
Db 5289 TTACATGAGTCTGTGTGGAGAGAGCCATAGGCTTACGCTGTTAAAGAGAGAGAGAGT 5348
Qy 5641 GGTGTAAGAAAGTCAAGACTTACATAGAGGCTAGCCACACGAAATGACAGACAGA 5700
Db 5349 GGTGTAAGAAAGTCAAGACTTACATAGAGGCTAGCCACACGAAATGACAGACAGA 5408
Qy 5701 TCCCTCTATCTCCCAATTAAGATTGAGTGCAC 5735
Db 5409 TCCCTCTATCTCCCAATTAAGATTGAGTGCAC 5443

RESULT 3
ABL49724
ID ABL49724 standard; DNA; 5443 BP.
XX
XX ABL49724;
XX
XX 29-MAY-2002 (first entry)
XX
XX Mouse promoter DNA sequence SEQ ID NO:2.
XX
XX DE
XX Human; p300; p300 transgenic animal; promoter; heart muscle cell;
XX KM
XX cardiant; heart failure; megalo-cardia; mouse; ds.
XX
XX Mus musculus.
XX
XX PN
XX WO200205633-A1.
XX
XX PD
XX 24-JAN-2002.
XX
XX PF
XX 13-JUL-2001; 2001WO-JP006086.
XX
XX PR
XX 14-JUL-2000; 2000JP-00215143.

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Db 1681 CTGTGCAACAGAGGTCGAGGACTGTGTAGAGCTTCAAGTAATGATGTCTCAAG 1740
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Db 1741 ATGGGGGGGGGGGGGATTTCTGGGGGGGGGAGAGAGGTGGAAGGAGCCCTGGAACAG 1800
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QY 1861 TAAATCATGAAGACAGAGGGAAGGGAAGCTGGAAGAGTGAAGAGACCCCGGGGCAAGA 1920
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Db 4809 CTTCCTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4868
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Db 4869 CTGTGTCAAGTGTGAGATCAACCTGGGGTCCCACTTATATTAACAATCTTCCA 4928
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QY 5581 TTACATGAGATCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5640
Db 5289 TTACATGAGATCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5348
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Db 5409 TCCCTCTATCTCTCCCATTAAGTTTGAAGTGAAC 5443

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RESULT 4

AAT31006
ID AAT31006 standard; DNA; 1679 BP.

AC AAT31006;

DT 26-SEP-1996 (first entry)

DE Mouse cardiac alpha myosin heavy chain promoter.

KM Gene therapy; hypoxia related enhancer element; HREB; Ischemia;
reperfusion; promoter; alpha myosin heavy chain; alpha-MHC; de.

OS Mus sp.

PN W09620276-A1.

PD 04-JUL-1996.

PF 13-NOV-1995; 95MO-IB000996.

XX

QY 5567 GAGAGGAGGACCTTTATCATGAGTCTGTGGAGAGCCATAGAGCTACCGGTGTAAGA 5626
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DB 1509 GAGAGGAGGACCTTTATCATGAGTCTGTGGAGAGCCATAGAGCTACCGGTGTAAGA 1568
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QY 5627 GGCAGGGAATGTGTGTGTGAGAAAGTCAGAGCTTCAATAGAAAGCTACCCACACAG 5686
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DB 1569 GGCAGGGAATGTGTGTGTGAGAAAGTCAGAGCTTCAATAGAAAGCTACCCACACAG 1628
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QY 5687 AAATGACAGACAGATCCCTCTATCTCCCATTAAGATTGAGT 5731
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DB 1629 AAATGACAGACAGATCCCTCTATCTCCCATTAAGATTGAGT 1673
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RESULT 5
ABV74357
ID ABV74357 standard; DNA; 1679 BP.
AC ABV74357;
XX
XX 05-FEB-2003 (first entry)
DT
XX Mouse cardiac alpha-myosin heavy chain promoter fragment.
DE
XX Therapeutic delivery system; electrical pulse generator; brain;
KM electrically responsive promoter; ischemic injury; cardiac; kidney;
KM arterial occlusive disease; coronary arterial disease; stroke; mouse;
KM alpha myosin; promoter; de.
XX
OS Mus sp.
XX WO200249669-A2.
PN
XX 27-JUN-2002.
PD
XX 20-DEC-2001; 2001WO-US049845.
PF
XX 21-DEC-2000; 2000US-0257460P.
PR 20-AUG-2001; 2001US-0313926P.
XX
XX (MEDT) MEDTRONIC INC.
PA
XX Schu CA, Padua R, Bonner M, Donovan MG, Soykan O;
PI
XX WPI: 2002-537680/57.
DR
XX Therapeutic delivery system used for treating e.g. peripheral arterial
PT occlusive disease or stroke comprises electrical pulse generator operably
PT coupled with genetically engineered cells in mammalian tissue.
XX
XX Disclosure; Page: 66pp + Sequence Listing; English.
XX
XX The invention relates to a therapeutic delivery system comprising an
CC electrical pulse generator operably coupled with genetically engineered
CC cells in a mammalian tissue. The genetically engineered cells also
CC comprise a target gene operably coupled to an electrically responsive
CC promoter. The delivery system is useful for the production of
CC therapeutically useful gene or protein products, in repairing tissue
CC injury (e.g. ischaemic injury, damaged cardiac tissue, kidney tissue,
CC brain tissue or endothelial tissue), in stimulating cells for controlled
CC expression of therapeutically useful gene and protein sequences and for
CC treating peripheral arterial occlusive disease, coronary arterial disease
CC or stroke. The present sequence is that of the mouse cardiac alpha-myosin
CC heavy chain promoter fragment, exemplary of cardiac specific promoter
CC regions. Note: The sequence data for this patent is not represented in
CC the printed specification but is based on sequence information supplied
CC to Derwent by the European Patent Office
CC
XX Sequence 1679 BP; 342 A; 486 C; 418 G; 433 T; 0 U; 0 Other;
SQ
Query March 22.3%; Score 1279.8; DB 6; Length 1679;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 1616; Conservative 0; Mismatches 57; Indels 292; Gaps 1;

QY 3767 GAATTCCTTACTATCAAAAGGAAAGTGAAGCTGACCTGCAAAAGTGTCTCCCT 3826
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DB 301 GGGTAGGAGAGTGTGTGAGAGCAGCTCTGTCTCTCTGATGCTGAGGCTGAGGCTTTG 360
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QY 4127 GGGAGAGGAAATGTGCCCAGAGCTAAATAAAGGAGGAGGAGGAGGAGGAGGAG 4186
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DB 526 ----- 525
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DB 526 ----- 525
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DB 526 ----- 525
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| | | | |
QY 4787 GACAGGATGAGCTTCAACAGAGCTGAGAGTTCAGTGGCAGAGAGTTTCCACAAAGAA 4846
| | | | |
DB 729 GACAGGATGAGCTTCAACAGAGCTGAGAGTTCAGTGGCAGAGAGTTTCCACAAAGAA 788
| | | | |

QY	4447	CACGTGATGCCCTTCCTTACGCTGTCCTTCACTCTTCTCTGGGAGATGTCCTCC	4908
Db	789	CACGTGATGCCCTTCCTTACGCTGTCCTTCACTCTTCTCTGGGAGATGTCCTCC	848
QY	4907	CGCTGTGGTTATCTGGGCTCTTGCTGTGAGCAAGATTGCGGTGCTCCACTCCA	4966
Db	849	CGCTTTGGTTTATCTTGGCTCTTGCTGTGAGCAAGATTGCGGTGCTCCACTCCA	908
QY	4967	TCTTTCTCTACTGTCCTCGTGCCTTGGCCCTTTCCTTTCGCTGTCCTTCCACCCA	5026
Db	909	TCTTTCTCTACTGTCCTCGTGCCTTGGCCCTTTCCTTTCGCTGTCCTTCCACCCA	968
QY	5027	TTTCTCACTTCACTTTTCTTCCCTCTGTCATTGTGATTCATCTTCTCTTCTTCT	5086
Db	969	TTTCTCACTTCACTTTTCTTCCCTCTGTCATTGTGATTCATCTTCTCTTCTTCT	1028
QY	5087	TCTCTTCCTTCCTTCCTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	5146
Db	1029	TCTCTTCCTTCCTTCCTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1088
QY	5147	TCTTTCTCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT	5206
Db	1089	TCTTTCTCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT	1148
QY	5207	TAAACAATCTTCCAGTGAACAACAAGCTTCAGTGTCTGTGGTGTCTTACTTCTCA	5266
Db	1149	TAAACAATCTTCCAGTGAACAACAAGCTTCAGTGTCTGTGGTGTCTTACTTCTCA	1208
QY	5267	CCCCCTGGCTTGTCTGTTCATCTGTGTGAGATCTCTAATTTGTCTCCACCTCTG	5326
Db	1209	CCCCCTGGCTTGTCTGTTCATCTGTGTGAGATCTCTAATTTGTCTCCACCTCTG	1268
QY	5327	CTACTCTCTTCTTCGCTGTCCTCTCTCTCTGACGTCGCGCACTGTGTCCTCTTC	5386
Db	1269	CTACTCTCTTCTTCGCTGTCCTCTCTCTCTGACGTCGCGCACTGTGTCCTCTTC	1328
QY	5387	CAGCTGTGTGTCACATTTCTTGAGATTTCTGTAAAGATTAAACAAGTGAATTTTCC	5446
Db	1329	CAGCTGTGTGTCACATTTCTTGAGATTTCTGTAAAGATTAAACAAGTGAATTTTCC	1388
QY	5447	CTGTAGACAGAGATTCACGATTTCTCCGGAAAGTCAGGCTTTCAGCCCTCTTCTCTGC	5506
Db	1389	CTGTAGACAGAGATTCACGATTTCTCCGGAAAGTCAGGCTTTCAGCCCTCTTCTCTGC	1448
QY	5507	CCAGCTGCCCGGCACTCTTACCAAACTCAGAGCACTTACCCGACATPAGACTCTGACA	5566
Db	1449	CCAGCTGCCCGGCACTCTTACCAAACTCAGAGCACTTACCCGACATPAGACTCTGACA	1508
QY	5567	GAGAGACAGGCACTTTTACATGAGTCTCTGTGTGGAGAGCCATPAGCTTACGGTGTAAAGA	5626
Db	1509	GAGAGACAGGCACTTTTACATGAGTCTCTGTGTGGAGAGCCATPAGCTTACGGTGTAAAGA	1568
QY	5627	GGCAGGGGAAGTGTGTGTGTAGAAAAGTCAGACTTCATATGAAGCCCTAGGCCACACAG	5686
Db	1569	GGCAGGGGAAGTGTGTGTGTAGAAAAGTCAGACTTCATATGAAGCCCTAGGCCACACAG	1628
QY	5687	AAATGACAGACAGATTCCTCTATCTCCCGCATPAGATTGTGAAT 5731	
Db	1629	AAATGACAGACAGATTCCTCTATCTCCCGCATPAGATTGTGAAT 1673	
RESULT 6			
ADL14241			
ID	ADL14241	standard; DNA; 1679 BP.	
XX	ADL14241;		
AC			
XX	06-MAY-2004	(first entry)	
DT			
XX			
DE			
Mouse		cardiac alpha-myosin heavy chain promoter region.	
Mouse		cardiac alpha-myosin heavy chain promoter; ds;	
TM		electrical pulse generator; electrically responsive promoter;	

KM	electrical response enhancer element; pacemaker.
XX	
XX	
OS	Mus sp.
XX	
XX	
PN	US2003204206-A1.
XX	
XX	
PD	30-OCT-2003.
XX	
XX	
PF	20-DEC-2001; 2001US-00027655.
XX	
XX	
PR	21-DEC-2000; 2000US-0257460P.
PR	20-AUG-2001; 2001US-0313926P.
XX	
XX	
PA	(MEDT) MEDTRONIC INC.
XX	
XX	
PI	Padua RA, Schu CA, Bonner MD, Donovan MG, Soykan O;
XX	
XX	
DR	WPI; 2004-032680/03.
PT	
PT	Therapeutic delivery system useful for regulating delivery of therapeutic
PT	proteins and nucleic acids, comprises electrical pulse generator coupled
PT	with genetically engineered cells in mammalian tissue.
XX	
XX	
PS	Disclosure; SEQ ID NO 5; 39pp; English.

CC The invention relates to a therapeutic delivery system comprising an
CC electrical pulse generator coupled with genetically engineered cells in
CC mammalian tissue. The genetically engineered cells further include a
CC target gene coupled to an electrically responsive promoter. The invention
CC also relates to an expression vector comprising an electrical response
CC enhancer element, a tissue specific promoter heterologous to the element
CC and a coding sequence, an apparatus for testing cells comprising an upper
CC plate electrode, a lower plate electrode and a porous membrane positioned
CC between electrodes during operation, and a method of treating a patient
CC comprising providing the patient with an electrical pulse generator
CC coupled with genetically engineered cells in a patient tissue. The
CC electrical pulse generator is a pacemaker. The method is used for
CC regulating the delivery of therapeutic proteins and nucleic acids. The
CC invention provides controlled and local delivery of therapeutically
CC important gene or protein products. This sequence represents the mouse
CC cardiac alpha-myosin heavy chain promoter region, used in the method of
CC the invention.

XX
XX
SQ Sequence 1679 BP, 342 A, 486 C, 418 G, 433 T, 0 U, 0 Other;

Query Match 22.3%; Score 1279.8; DB 12; Length 1679;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 1616; Conservative 0; Mismatches 57; Indels 292; Gaps 1;

QY	3767	GAATTCCTTATCTATTCAAAGGGAACCTGAGTCGCGACCTGCAAAAGTGATTCCTCCTCCT	3826
Db	1	GAATTCCTTATCTATTCAAAGGGAACCTGAGTCGCGACCTGCAAAAGTGATTCCTCCTCCT	60
QY	3827	AGACATCATGACTTTCCTCTCGGGGAGCCAGCACTGTGAACTTCAGAGCTTGAGAGAGTA	3886
Db	61	AGACATCATGACTTTCCTCTCGGGGAGCCAGCACTGTGAACTTCAGAGCTTGAGAGAGTA	120
QY	3887	GGAGGCTCCCTCAGCCTGAAGCTATGCAATGACCAGGGTTGAAAAGGAGGAAAGGAGAG	3946
Db	121	GGAGGCTCCCTCAGCCTGAAGCTATGCAATGACCAGGGTTGAAAAGGAGGAAAGGAGAG	180
QY	3947	CTGCGAATGGAGAGTTTCCTGCTTGGAGGAGGAGGAGACGATATTTAAGCTGGAAGAGAGG	4006
Db	181	CTGCGAATGGAGAGTTTCCTGCTTGGAGGAGGAGGAGACGATATTTAAGCTGGAAGAGAGG	240
QY	4007	TGACCCCTTACCCAGATGTTCACTACACCTTCAGATTAATAAATACTGAGGTAAAGGCGCT	4066
Db	241	TGACCCCTTACCCAGATGTTCACTACACCTTCAGATTAATAAATACTGAGGTAAAGGCGCT	300
QY	4067	GGGTAGGGGAGGTGTGTGAGACGCTCTGTCTCTCTCTGCAATGCCCTTGAAGGCCCTTTTG	4126
Db	301	GGGTAGGGGAGGTGTGTGAGACGCTCTGTCTCTCTCTCTGCAATGCCCTTGAAGGCCCTTTTG	360

QY	4127	GGGAGGAGAAATGAGCCCAAGACCTAAAAAAAGGCATATGAGCCAGAGGGGCGAGGCCAA	4186
Db	361	GGGAGGAGAAATGAGCCCAAGACCTAAAAAAAGGCATATGAGCCAGAGGGGCGAGGCCAA	420
QY	4187	CAGACCTTCTATGAGGCAAACTTGGGGCCCGTAGTGAATGATTAACAAGAACTGGCAAT	4246
Db	421	CAGACCTTCTATGAGGCAAACTTGGGGCCCGTAGTGAATGATTAACAAGAACTGGCAAT	480
QY	4247	CGATACCTTCTTCTTCTTAACGAGCAGAGAGGAACTCGAGTTTACCACTCCTCATGAGT	4306
Db	481	GGATCAAAAGAGAGAGAGCCAGAGCAGAGAGGAAAGTGGAGAGGAG-----	525
QY	4307	ATTAGAGAAAGATGAAAGTCGAGTTTACACCTCCATCAGATGATAGAGAAAGTGAAGT	4366
Db	526	-----	525
QY	4367	CGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAAGTCGATTTACCACTCCCTA	4426
Db	526	-----	525
QY	4427	TCAGTATAGAGAAAAGTGAAGTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGT	4486
Db	526	-----	525
QY	4487	GAAAGTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAGTGAAAGTCGAGTTTACCA	4546
Db	526	-----	525
QY	4547	TCCTTATCAGTATAGAGAAAAGTGAAGTCGAGTCGGTACACAGAGAGACTCCAAT	4606
Db	526	-----	525
QY	4607	TTAGGACAGAGCANTATGGAGTGGATTTAAAGGGCTGAGCACTGAGACTGTCAAG	4666
Db	549	TTAGGACAGAGCANTATGGAGTGGATTTAAAGGGCTGAGCACTGAGACTGTCAAG	608
QY	4667	ATTTCCTCCAAACCCAGGTAAAGAGAGATTTCGGGTGGGGGCTTCCACCCACAGACCT	4726
Db	609	ATTTCCTCCAAACCCAGGTAAAGAGAGATTTCGGGTGGGGGCTTCCACCCACAGACCT	668
QY	4727	CTCCCACTTGAAGAGAAACTGCGCTTCTGAGAAAGTGGGTTCAAGGCCGGTCAGAGATCT	4786
Db	669	CTCCCACTTGAAGAGAAACTGCGCTTCTGAGAAAGTGGGTTCAAGGCCGGTCAGAGATCT	728
QY	4787	GACAGGGTGGCTTCCACAGACCTGGGAAAGTTCTCAGTGGCAGAGAGGTTTCCAAAGAAA	4846
Db	729	GACAGGGTGGCTTCCACAGACCTGGGAAAGTTCTCAGTGGCAGAGAGGTTTCCAAAGAAA	788
QY	4847	CACGTGAGTCCCTTCCCTTACGCTGTCTTCCATCTTCTCTCTGGGGAGTGTCTCTCC	4906
Db	789	CACGTGAGTCCCTTCCCTTACGCTGTCTTCCATCTTCTCTCTGGGGAGTGTCTCTCC	848
QY	4907	CGTCTGAGTTATCTTGGCTCTTGCCTTTCAGACAAAGTTTGCCCGTGTCTTCCACTCCA	4966
Db	849	CGTCTGAGTTATCTTGGCTCTTGCCTTTCAGACAAAGTTTGCCCGTGTCTTCCACTCCA	908
QY	4967	TCCTTCTCTACTGTCTCCGTGCTTGCCTTGCCTTTCGAGTGTCTTCTTTCCACCCA	5026
Db	909	TCCTTCTCTACTGTCTCCGTGCTTGCCTTGCCTTTCGAGTGTCTTCTTTCCACCCA	968
QY	5027	TTTTCTCATTCACCTTTTCTCCCTTCTTCATTTGTATTATCATCTTCTCTCTCTCTCT	5086
Db	969	TTTTCTCATTCACCTTTTCTCCCTTCTTCATTTGTATTATCATCTTCTCTCTCTCTCT	1028
QY	5087	TCCTTCCCT	5146
Db	1029	TCCTTCCCT	1088
QY	5147	TCCTTCCCT	5206
Db	1089	TCCTTCCCT	1148
QY	5207	TAAACAATCTTCCAGTGAAGCAACAGCTTCAAGTGTCTGGGTCTCTTTCACCTTCTCA	5266

[illegible]

```

RESULT 7
ADSS97705
ID ADS97705 standard; DNA; 5190 BP.
XX
XX AC ADS97705;
XX
XX DT 16-DEC-2004 (first entry)
XX
XX DE Rabbit alpha-myosin heavy chain promoter.
XX
XX KW Rabbit; alpha-myosin; promoter; transgenic; cardiomyopathy; cardiant; ds
XX
XX OS Oryctolagus cuniculus.
XX
XX PN WO2004082370-A2.
XX
XX PD 30-SEP-2004.
XX
XX PE 12-MAR-2004; 2004WO-US007740.
XX
XX PR 13-MAR-2003; 2003US-0454947P.
XX
XX PR 11-MAR-2004; 2004US-01122334.
XX
XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
XX PI Robbins J;
XX
XX DR WPI; 2004-718695/70.
XX
XX PT New animal cell that is stably transformed with an expression cassette
XX
XX PT comprising a promoter and a heterologous nucleotide sequence operably
XX
XX PT linked to the promoter, useful in identifying anti-cardiopathic
XX
XX PS Claim 1; SEQ ID NO 1; 8pp; English.
XX
XX CC The present sequence is that of the rabbit alpha-myosin heavy chain gene

```


Db 3846 TGGAGAGGCTAGGCGCAAGAGGAGGAACTGCAGCTGGGGGCGAGGAGCAAGCATTC 3905
 QY 3991 AGCCTGGAAGAAGAGGACCTTACCCAGTGTG--TCACCTACACCTTTCAGATTAAAA 4048
 Db 3906 GTCCTATATATAAAGAGGACCTCACTCCAGTGTGCTCAACCTTAAAGTTAAAA 3965
 QY 4049 TAACTGAGTAAAGGCTGGGTAGGAGGTGTGT----GAGACGCTCTGTCTCTCT 4104
 Db 3966 TAACCGAGTAAAGCCATGTGGGGCGGGAGGTGTGTAGAGAGGTCTGTCTTCCCA 4025
 QY 4105 CTGCAATCCCTGAGGCTTTGGGAGAGAGATGTGCCAGACTTAAAAAAGGCCAT 4164
 Db 4026 CTATCTGCCATCAGCGCTCTGGAGGGCGGAAATGTCTCAAGACTTAAAAAAGGCCCT 4085
 QY 4165 GAGAGCCGAGGGGCGAGGAGCAAGACCTTCATGGGCAAACTGGGGGCC 4216
 Db 4086 GAGAGCCGAGGGGCTGGGGAGAGACCTTTCATGGGCAAACTGGGGGCC 4137

RESULT 8

ID AAT11359 standard; DNA; 520 BP.

AC AAT11359;

DT 07-JUL-1996 (first entry)

DE Bidirectional promoter.

KM Tet repressor; Herpes simplex virus; HSV; virion protein 16; VP16; fusion protein; gene expression; regulation; inhibition; activation; transcription; ds.

OS Synthetic.

PN MO9601313-A1.

PD 18-JAN-1996.

PF 29-JUN-1995; 95MO-US008179.

PR 01-JUL-1994; 94US-00270637.

PR 15-JUL-1994; 94US-00275876.

PR 03-FEB-1995; 95US-00383754.

PR 07-JUN-1995; 95US-00486814.

PA (BUJAR) BUJAR H.

PI (GOSSEN) GOSSEN M.

PI Bujard H, Gossen M;

DR WPI; 1996-087666/09.

PS New tetracycline-regulated transcription modulators - comprising fusion

PT proteins which bind to tet operator sequences to activate or inhibit

PT transcription.

PT Disclousure; Page 73; 112pp; English.

XX Fusion proteins comprising a first polypeptide which binds to a tet

XX operator sequence in the presence of tetracycline or a tetracycline

XX analogue, operatively linked to a second polypeptide which either

XX activates or inhibits transcription in eukaryotic cells may be used to

XX activate or inhibit transcription. Such proteins may be used to regulate

XX gene expression in cells and may be particularly useful for gene therapy

XX and for expression of gene products in transgenic organisms. Induction of

XX gene expression is rapid, efficient and strong, typically 1000-2000 fold.

XX The inducing agent does not cause pleiotropic effects or cytotoxicity in

XX eukaryotic cells. This sequence is a bidirectional promoter which can be

XX used in the production of vector constructs. See also AAT11358

XX Sequence 520 BP; 152 A; 122 C; 131 G; 115 T; 0 U; 0 Other;

Query Match 5.4%; Score 311.8; DB 2; Length 520;
 Best Local Similarity 99.4%; Pred. No. 8.7e-78;
 Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4277 GGAATCGAATTACCACTCCCTATGATGATAGAGAAAAGTGAAGTGAAGTTACCA 4336
 Db 63 GGATCTCGAGTTTACCACTCCCTATGATGATAGAGAAAAGTGAAGTGAAGTTACCA 122
 QY 4337 TCCCTATGATGATGAGAAAAGTGAAGTGAAGTGAAGTTACCACTCCCTATGATGAT 4396
 Db 123 TCCCTATGATGATGAGAAAAGTGAAGTGAAGTGAAGTTACCACTCCCTATGATGAT 182
 QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATGATGATGATGAGAAAAGTGAAGTT 4456
 Db 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATGATGATGATGAGAAAAGTGAAGTT 242
 QY 4457 TACCACTCCCTATGATGATGAGAAAAGTGAAGTGAAGTGAAGTTTACCACTCCCTATGATG 4516
 Db 243 TACCACTCCCTATGATGATGAGAAAAGTGAAGTGAAGTGAAGTTTACCACTCCCTATGATG 302
 QY 4517 ATGAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATGATGATGAGAAAAGTGAAGT 4576
 Db 303 ATGAGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATGATGATGAGAAAAGTGAAGT 362
 QY 4577 CGAGCTCGGTACCG 4591
 Db 363 CGAGCTCGGTACCG 377

RESULT 9

ID AAT45722 standard; DNA; 520 BP.

AC AAT45722;

DT 18-MAR-1997 (first entry)

DE Bi-directional tetracycline-regulated promoter region.

KM Tet; tetracycline; Tet; operator; transcription; regulation; inducible; repressor; gene expression; therapy; transgenic animal; disease model; HSV; herpes simplex virus; tk; thymidine kinase; ds.

OS Synthetic.

FT Key Location/Qualifiers

FT promoter 24..427

FT /*tag= a

FT /note= "bi-directional, i.e. translation starts in a 3' to 5' direction at posn. 24 and translation starts in 5' to 3' direction at posn. 427, an explanatory figure is given in the specification"

FT repeat_region 69..363

FT /*tag= b

FT /rpt_type= direct

FT /note= "seven repeats of the tet operator sequence contained within the bi-directional promoter"

PN MO9640892-A1.

PD 19-DEC-1996.

PF 06-JUN-1996; 96MO-US009049.

PR 07-JUN-1995; 95US-00485971.

PA (BADI) BASF AG.

PI Bujard H, Gossen M, Hillen W, Helbl V, Schnappinger D;

DR WPI; 1997-052305/05.

PT Nucleic acid encoding tetracycline-inducible transcription regulatory
 PT fusion protein - comprising modified tetracycline repressor able to bind
 PT mutant tet operator fused to transcription regulator, useful for
 PT modulating eukaryotic gene expression.
 PS Disclosure; Page 79-80; 117pp; English.
 XX
 CC AAT45721 and AAT45722 are bi-directional, tetracycline (Tc)-regulated
 CC promoters used to co-ordinate regulation of expression of 2 genes of
 CC interest. The promoters contain tet operator sequences and a minimal
 CC herpes simplex virus (HSV) thymidine kinase (tk) promoter. The main
 CC invention of the specification concerns modified Tet repressor (Tetr)
 CC proteins that bind to modified class B tet operator sequences tetrO-4C and
 CC tetrO-6C (see AAT45711 and AAT48478). Modified Tetr proteins can be fused
 CC to any transcription regulatory polypeptide (e.g. HSV virion protein 16,
 CC VP16) and used to control transcription of a tetrO-4C or tetrO-6C linked
 CC gene. Nucleic acid encoding such a fusion protein may be introduced into
 CC a cell and transcription of the protein can be controlled by altering the
 CC concn. of tetracycline (or an analogue) in the cell, as appropriate. This
 CC ability to modulate gene expression in a predictable way is very useful
 CC in gene therapy and for recombinant protein prodn. in cultured cells or
 CC transgenic animals. The Tc-inducible system is also useful for the prodn.
 CC of transgenic animal models for the study of disease and also for the
 CC study of gene function e.g. during differentiation. The Tc-inducible
 CC system allows rapid activation of gene transcription without cellular
 CC toxicity, high concns. of inducer are not required
 XX
 SQ Sequence 520 BP; 152 A; 122 C; 131 G; 115 T; 0 U; 0 Other;
 XX
 Query Match 5.4%; Score 311.8; DB 2; Length 520;
 Best Local Similarity 99.4%; Pred. No. 8.7e-78;
 Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4277 GGAAGTCGAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCAAC 4336
 DB 63 GGATCTCGAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCAAC 122
 QY 4337 TCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAG 4396
 DB 123 TCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAG 182
 QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTT 4456
 DB 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTT 242
 QY 4457 TACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTG 4516
 DB 243 TACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTG 302
 QY 4517 ATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGT 4576
 DB 303 ATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGT 362
 QY 4577 CGAGCTCGGTACGAG 4591
 DB 363 CGAGCTCGGTACCG 377
 RESULT 10
 AAV60079
 ID AAV60079 standard; DNA; 520 BP.
 XX
 AC AAV60079;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-DEC-1998 (first entry)
 XX
 DE Bidirectional promoter region for coordinate regulation of 2 genes.
 XX
 KW Tet repressor; tetracycline; regulation; expression;
 KW Tet operator-linked gene; bidirectional promoter region;
 KW coordinate regulation; tetracycline-regulated transcriptional activator;
 KW db.

XX
 OS Synthetic.
 XX
 PN US5814618-A.
 XX
 XX 29-SEP-1998.
 PF 07-JUN-1995; 95US-00485978.
 PR 14-JUN-1993; 93US-00076327.
 PR 14-JUN-1993; 93US-00076726.
 PR 14-JUN-1994; 94US-00260452.
 PR 01-JUL-1994; 94US-00270637.
 PR 15-JUL-1994; 94US-00275876.
 PR 03-FEB-1995; 95US-00383754.
 XX
 PA (KNOL) KNOL AG.
 PA (BADI) BASF AG.
 XX
 PI Gossen M, Bujard H;
 DR WPI; 1998-541795/46.
 XX
 PT Tetracycline based regulation of gene expression - uses a tetracycline
 PT operator sequence joined to a gene of interest, the gene of interest
 PT being induced in the presence, but not absence of the antibiotic.
 XX
 PS Disclosure; Fig 7B; 63pp; English.
 XX
 SQ The present sequence represents a bidirectional promoter region for
 CC coordinate regulation of 2 genes by a tetracycline-regulated
 CC transcriptional activator. The specification describes a method for
 CC regulating expression of a Tet (tetracycline) operator-linked gene in a
 CC cell of a subject. The method comprises introducing into the cell a
 CC nucleic acid encoding a fusion protein which inhibits transcription in
 CC eukaryotic cells, the fusion protein comprising a polypeptide which binds
 CC to a Tet operator sequence, operatively linked to heterologous second
 CC polypeptide which inhibits transcription in eukaryotic cells and
 CC modulating the concentration of a tetracycline (analogue) in the subject.
 CC The method is used for the regulation of gene expression system, using
 CC tetracycline (analogues). The system enables a gene coupled to the system
 CC to be induced in the presence of Tet and then stopped when Tet is
 CC removed. (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 520 BP; 152 A; 122 C; 131 G; 115 T; 0 U; 0 Other;
 XX
 Query Match 5.4%; Score 311.8; DB 2; Length 520;
 Best Local Similarity 99.4%; Pred. No. 8.7e-78;
 Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4277 GGAAGTCGAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCAAC 4336
 DB 63 GGATCTCGAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCAAC 122
 QY 4337 TCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAG 4396
 DB 123 TCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAG 182
 QY 4397 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTT 4456
 DB 183 AAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTT 242
 QY 4457 TACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTG 4516
 DB 243 TACCACTCCCTATCAGTATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTG 302
 QY 4517 ATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGT 4576
 DB 303 ATGAGAAAAGTGAAGTGAAGTTTACCACTCCCTATCAGTATGAGAAAAGTGAAGT 362
 QY 4577 CGAGCTCGGTACGAG 4591
 DB 363 CGAGCTCGGTACCG 377

expression in a cell, using tetracycline-regulated fusion proteins. The method involves obtaining a cell from a subject, and introducing a nucleic acid molecule into the cell, which operatively links a gene to at least one tetracycline (tet) operator sequence. A second nucleic acid molecule is then introduced which encodes a fusion protein, where the fusion protein comprises a first polypeptide which binds to a tet operator sequence in the presence of tetracycline, or its analogue, operatively linked to a second polypeptide (e.g. Vp16) which activates transcription in eukaryotic cells to form a modified cell. The modified cell can then be administered to the subject, and the concentration of tetracycline (or and analogue) can be regulated so that the expression of the gene is regulated. The method is useful for gene therapy of diseases such as cancer and arthritis or for tissue regeneration and wound healing. The method may also be useful for the production of proteins in vitro and in vivo and for the production of stable cell lines for cloning

XX Sequence 520 BP; 152 A; 122 C; 131 G; 115 T; 0 U; 0 Other;

Query Match 5.4%; Score 311.8; DB 3; Length 520;
Best Local Similarity 99.4%; Pred. No. 8.7e-78;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4277 GGAAGTGGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCA 4336
DB 63 GGATCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCA 122
QY 4337 TCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAG 4396
DB 123 TCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAG 182
QY 4397 AAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTT 4456
DB 183 AAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTT 242
QY 4457 TACCACCTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGT 4516
DB 243 TACCACCTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGT 302
QY 4517 ATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGT 4576
DB 303 ATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGT 362
QY 4577 CGAGCTCGGTACCAG 4591
DB 363 CGAGCTCGGTACCAG 377

RESULT 13
AAH47631 standard; DNA; 520 BP.

XX AAH47631;
XX
XX 30-NOV-2001 (first entry)
XX
DE Nucleotide sequence of a bidirectional promoter region.
XX
XX Fusion protein; tet operator; tetracycline; gene therapy; anti-cancer;
XX rheumatoid arthritis; hypopituitarism; wound healing; hemophilia;
XX diabetes; Alzheimer's disease; tet repressor; promoter; ds.
XX
XX Unidentified.
XX
XX US6271348-B1.
XX
XX 07-AUG-2001.
XX
XX 24-JAN-2000; 2000US-00489777.
XX
XX 14-JUN-1993; 93US-00076726.
XX 19-JUN-1993; 93US-00076327.
XX 14-JUN-1994; 94US-00260452.
XX 01-JUL-1994; 94US-00270637.

PR 15-JUL-1994; 94US-00275876.
PR 03-FEB-1995; 95US-00383754.
PR 07-JUN-1995; 95US-00485978.
PR 28-SEP-1998; 98US-00162184.
XX
XX (BAD) BASF AG.
XX (KNOL) KNOLL AG.
XX
XX Bujard H, Gossen M;
XX WPI; 2001-556625/62.
XX
XX Fusion protein for inhibiting transcription in eukaryotic cells useful in
XX gene therapy applications comprises a first polypeptide, which binds to
XX tet operator sequences, operatively linked to a heterologous second
XX polypeptide.
XX
XX Disclosure; Fig 7B; 69pp; English.

CC The invention relates to a fusion protein that comprises a first
CC polypeptide which binds to tet operator sequences, operatively linked to
CC a heterologous second polypeptide, which inhibits transcription in
CC eukaryotic cells. The fusion proteins are tetracycline-responsive and are
CC useful for regulation of transcription in eukaryotic cells and animals.
CC The tetracycline (Tc)-controlled regulatory system is useful in various
CC applications in gene therapy, such as in the treatment of various disease
CC conditions e.g. rheumatoid arthritis, hypopituitarism, wound healing and
CC tissue regeneration, anticancer treatments, benign prostatic hypertrophy,
CC hemophilia, diabetes and atherosclerosis. They are also useful for bone
CC marrow support therapy, treatment of central nervous system disorders
CC e.g. Alzheimer's disease, Parkinson's disease (see AAH47628 for a
CC detailed description of the uses). The present sequence represents the
CC nucleotide sequence of a bidirectional promoter region for coordinate
CC regulation of two genes of interest by tetracycline-regulated
CC transcriptional activator
XX
XX Sequence 520 BP; 152 A; 122 C; 131 G; 115 T; 0 U; 0 Other;

Query Match 5.4%; Score 311.8; DB 4; Length 520;
Best Local Similarity 99.4%; Pred. No. 8.7e-78;
Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4277 GGAAGTGGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCA 4336
DB 63 GGATCTCGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCA 122
QY 4337 TCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAG 4396
DB 123 TCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAG 182
QY 4397 AAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTT 4456
DB 183 AAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTT 242
QY 4457 TACCACCTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGT 4516
DB 243 TACCACCTCCCTATCAGTATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGT 302
QY 4517 ATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGT 4576
DB 303 ATAGAGAAAGTGAAGTGGAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGT 362
QY 4577 CGAGCTCGGTACCAG 4591
DB 363 CGAGCTCGGTACCAG 377

RESULT 14
AAH25572 standard; DNA; 520 BP.

XX AAH25572;
XX
XX 14-JUN-1994; 94US-00270637.
XX 01-JUL-1994; 94US-00270637.

DT 05-SEP-2001 (first entry)
 XX Nucleotide sequence of a bidirectional promoter.
 DE
 XX Transgenic plant; transgene; tet operator-linked gene; Tet repressor;
 KM tetracycline-regulated transcriptional regulatory system; tet operator;
 KW tetracycline; ds.
 XX
 OS Unidentified.
 XX
 PN US6242667-B1.
 XX
 PD 05-JUN-2001.
 XX
 XX 28-SEP-1998; 98US-00161902.
 PF
 XX 14-JUN-1993; 93US-00076327.
 PR 14-JUN-1993; 93US-00076726.
 PR 14-JUN-1994; 94US-00260452.
 PR 01-JUL-1994; 94US-00270637.
 PR 15-JUL-1994; 94US-00275876.
 PR 03-FEB-1995; 95US-00383754.
 PR 07-JUN-1995; 95US-00487472.
 XX
 PA (BADT) BASF AG.
 PA (KNOL) KNOLL AG.
 PI
 PI Bujard H, Gossen M;
 XX
 XX WPI; 2001-396837/42.
 DR
 XX Transgenic plant for regulating the expression of genes, comprises a
 PT transgene integrated into the genome and a tet operator-linked gene in
 PT the genome.
 XX
 XX Disclosure; Fig 7B; 65pp; English.
 PS
 XX The specification describes a transgenic plant with a tetracycline-
 CC regulated transcriptional regulatory system. The transgenic plants have a
 CC transgene and a tet operator-linked gene integrated in the genome, which
 CC confers a detectable and functional phenotype on the plant when
 CC expressed. The transgene comprises a transcriptional regulatory element
 CC functional in cells of the plant operatively linked to a polynucleotide
 CC sequence encoding a fusion protein that activates transcription of the
 CC tet operator linked gene. The fusion protein comprises a first
 CC polypeptide that is a mutated Tet repressor that binds to a tet operator
 CC sequence in the presence of tetracycline or its analogue, operatively
 CC linked to a second polypeptide that activates transcription in eukaryotic
 CC cells. In the presence of tetracycline, the fusion protein binds to the
 CC tet operator-linked gene and activates transcription of the tet operator-
 CC linked gene such that it is expressed at a level sufficient to confer the
 CC detectable and functional phenotype on the plant. The level of expression
 CC of the tet-operator gene can be downmodulated by depleting tetracycline
 CC from the plant. The transgene can be used to regulate the expression of
 CC genes in the plant. The transgenic plant can be used to analyse the
 CC functions of cellular proteins. The present sequence represents a
 CC bidirectional promoter for coordinate regulation of two genes of interest
 CC by a tetracycline-regulated transcriptional activator. It is used to
 CC produce transgenic plants of the invention
 XX
 SO Sequence 520 BP; 152 A; 122 C; 131 G; 115 T; 0 U; 0 Other;
 Query Match 5.4%; Score 311.8; DB 5; Length 520;
 Best Local Similarity 99.4%; Pred. No. 8.7e-78;
 Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4277 GGAAGTCAAGTTTACCTCCCTATCAGTATAGAGAAAGTGAAGTGCAGTTTACAC 4336
 DB 63 GGATCTCGAGTTTACCTCCCTATCAGTATAGAGAAAGTGAAGTGCAGTTTACAC 122
 QY 4337 TCCCTATCAGTATAGAGAAAGTGAAGTGCAGTTTACCTCCCTATCAGTATAGAG 4396
 DB 123 TCCCTATCAGTATAGAGAAAGTGAAGTGCAGTTTACCTCCCTATCAGTATAGAG 182

QY 4397 AAAAGTGAAGTGCAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGCAGTT 4456
 DB 183 AAAAGTGAAGTGCAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGTGCAGTT 242
 QY 4457 TACCACTCCCTATCAGTATAGAGAAAGTGAAGTGCAGTTTACCACTCCCTATCAGTG 4516
 DB 243 TACCACTCCCTATCAGTATAGAGAAAGTGAAGTGCAGTTTACCACTCCCTATCAGTG 302
 QY 4517 ATAGAGAAAGTGAAGTGCAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGT 4576
 DB 303 ATAGAGAAAGTGAAGTGCAGTTTACCACTCCCTATCAGTATAGAGAAAGTGAAGT 362
 QY 4577 CGAGCTCGGTACCG 4591
 DB 363 CGAGCTCGGTACCG 377
 RESULT 15
 ACA94734
 ID ACA94734 standard; DNA; 520 BP.
 XX
 AC ACA94734;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 XX Tet coordinated bi-directional promoter region #2.
 DE
 XX Gene therapy; tet promoter; transgenic; rheumatoid arthritis; ds;
 KM hypopituitarism; wound healing; anti-cancer treatment; promoter;
 KW transgenic farm animal; stable cell line production; tetracycline.
 XX
 OS Unidentified.
 XX
 XX US2003022315-A1.
 PN
 PD 30-JAN-2003.
 PD
 XX 03-AUG-2001; 2001US-00921650.
 PF
 XX 14-JUN-1993; 93US-00076327.
 PR 01-JUL-1994; 94US-00270637.
 PR 15-JUL-1994; 94US-00275876.
 PR 03-FEB-1995; 95US-00383754.
 PR 07-JUN-1995; 95US-00485978.
 PR 28-SEP-1998; 98US-00162184.
 PR 24-JAN-2000; 2000US-00489777.
 XX
 PA (BADT) BASF AG.
 PA (KNOL) KNOLL AG.
 PI
 PI Bujard H, Gossen M;
 XX
 XX WPI; 2003-438975/41.
 DR
 XX Regulating expression of a gene in cell of a subject, by utilizing
 PT components of tetracycline repressor/operator inducer system of
 PT prokaryotes to regulate gene expression in eukaryotic cells.
 XX
 XX Disclosure; Fig 7B; 71pp; English.
 PS
 XX The invention relates to a method of regulating expression of a tet
 CC operator-linked gene in cell of a subject, which involves introducing
 CC into the cell a nucleic acid molecule encoding a fusion protein which
 CC inhibits transcription in eukaryotic cells, comprising a first
 CC polypeptide which binds to a tet operator sequence, operatively linked to
 CC a heterologous polypeptide which inhibits transcription in eukaryotic
 CC cells and modulating concentration of tetracycline, or its analogue in
 CC the subject. The method is useful for regulating expression of a
 CC exogenous or endogenous gene in a cell. The system has widespread
 CC applicability to the study of cellular development and differentiation in
 CC eukaryotic cells, plants and animals. For expression of e.g. oncogenes
 CC can be regulated in a controlled manner in cells to study their function.

CC The system can be used to regulate the expression of site-specific
CC recombinases such as CRE or Flp, to allow for irreversible modification
CC of the genotype of a transgenic organism under controlled conditions at a
CC particular stage of development. The method is also useful for gene
CC therapy purposes, in treatment for either genetic or acquired diseases,
CC including rheumatoid arthritis, hypopituitarism, wound healing and anti-
CC cancer treatments, for large-scale production of proteins in vitro and in
CC transgenic farm animals and for production of stable cell lines for gene
CC cloning. The present sequence represents DNA encoding a tet promoter
XX

Sequence 520 BP; 152 A; 122 C; 131 G; 115 T; 0 U; 0 Other;

Query Match 5.4%; Score 311.8; DB 8; Length 520;

Best Local Similarity 99.4%; Pred. No. 8.7e-78;

Matches 313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	4277	GGAACTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAGTCGAGTTTACCAAC	4336
DB	63	GGATCTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAGTCGAGTTTACCAAC	122
QY	4337	TCCTATCAGTGATAGAGAAAAGTGAAGTCGAGTTTACCACTCCCTATCAGTGATAGAG	4396
DB	123	TCCTATCAGTGATAGAGAAAAGTGAAGTCGAGTTTACCACTCCCTATCAGTGATAGAG	182
QY	4397	AAAAGTGAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAGTCGAGTT	4456
DB	183	AAAAGTGAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAGTCGAGTT	242
QY	4457	TACCACTCCCTATCAGTGATAGAGAAAAGTGAAGTCGAGTTTACCACTCCCTATCAGTG	4516
DB	243	TACCACTCCCTATCAGTGATAGAGAAAAGTGAAGTCGAGTTTACCACTCCCTATCAGTG	302
QY	4517	ATGAGAGAAAAGTGAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAGT	4576
DB	303	ATGAGAGAAAAGTGAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAGT	362
QY	4577	CGAGCTCGGTACCAG	4591
DB	363	CGAGCTCGGTACCG	377

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Job time : 1882 secs

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1 GGATCCTGCAAGTCAACAAAGGTCTCCACCACCAAGTGCCCTAGTCTCAATTTCAGT 60

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QY	2221	AAGGAAAGAAAGGGGCAAA	CCAGGCCACACAA	GAGGGCGAGACC	CCAGAACTGAATTAACTC	2280
Db	2221	AAGGAAAGAAAGGGGCAAA	CCAGGGCCACAA	GAGGGCGAGACC	CCAGAACTGAATTAACTC	2280
QY	2281	CTTCCTTGTTGCATCTTCTT	CCATPAGGAGGAGTGGGAA	CTCTGTGACAC	CAATCCCCCATGA	2340
Db	2281	CTTCCTTGTTGCATCTTCTT	CCATPAGGAGGAGTGGGAA	CTCTGTGACAC	CAATCCCCCATGA	2340
QY	2341	GGCCCCCACTACCCATAC	CCAGAGTTTGGCCTGAGTGG	CAATTCTAGGTTCCCTGAGACAGAG	2400	
Db	2341	GGCCCCCACTACCCATAC	CCAGAGTTTGGCCTGAGTGG	CAATTCTAGGTTCCCTGAGACAGAG	2400	
QY	2401	CTGTGGCCTTGTCTCTT	GTGAGACTGTACCCAACTGAC	CCAAATGTTTCTCACTGATCTTTGAAT	2460	
Db	2401	CTGTGGCCTTGTCTCTT	GTGAGACTGTACCCAACTGAC	CCAAATGTTTCTCACTGATCTTTGAAT	2460	
QY	2461	GGCCCTCAAGAGCTTGAAGA	CCAGGCAAGATATTAGGCGCAT	TGGGGCTTAACCCCTGAGAGCT	2520	
Db	2461	GGCCCTCAAGAGCTTGAAGA	CCAGGCAAGATATTAGGCGCAT	TGGGGCTTAACCCCTGAGAGCT	2520	
QY	2521	TGCAACACGAGAGCCTCAAG	TGACCTCCAGGAGACAGCTG	CAGACAGGTGGCCTTTATCC	2580	
Db	2521	TGCAACACGAGAGCCTCAAG	TGACCTCCAGGAGACAGCTG	CAGACAGGTGGCCTTTATCC	2580	
QY	2581	CCAAAAGAGCAACATTTGG	CAATPAGGTGCTGCAAT	TGGGAATGCAAGTTGAATCAGCTC	2640	
Db	2581	CCAAAAGAGCAACATTTGG	CAATPAGGTGCTGCAAT	TGGGAATGCAAGTTGAATCAGCTC	2640	
QY	2641	CCCTTCAAGAAATACATG	CAATGCAAGAACCCTTGAAG	AGAGGGGATATGCTCTCTGCC	2700	
Db	2641	CCCTTCAAGAAATACATG	CAATGCAAGAACCCTTGAAG	AGAGGGGATATGCTCTCTGCC	2700	
QY	2701	CCACCCCA	CCATPAGGGGAGTGA	CTATCTCTGAGGGGCTGCGAGAC	CTTTGGGAGACACAC	2760
Db	2701	CCACCCCA	CCATPAGGGGAGTGA	CTATCTCTGAGGGGCTGCGAGAC	CTTTGGGAGACACAC	2760
QY	2761	ATTACATGAGAGTGTG	CTGACCCAGAAAAC	CTGACCGCTGTGTCTTGCCAC	CTTCCAC	2820
Db	2761	ATTACATGAGAGTGTG	CTGACCCAGAAAAC	CTGACCGCTGTGTCTTGCCAC	CTTCCAC	2820
QY	2821	TCTTAGAGCTAAT	TGAGAGGTGACAGTGAAT	TAGGTTGGAGCTGTGAC	AGGAGAGTGT	2880
Db	2821	TCTTAGAGCTAAT	TGAGAGGTGACAGTGAAT	TAGGTTGGAGCTGTGAC	AGGAGAGTGT	2880
QY	2881	TCTGTGGGTGTGAGGGTGT	GAAGGAAAAGCCAGAC	AGGGGAGTCTGGCTTTGTCTCTGAA	2940	
Db	2881	TCTGTGGGTGTGAGGGTGT	GAAGGAAAAGCCAGAC	AGGGGAGTCTGGCTTTGTCTCTGAA	2940	
QY	2941	CACAAATGTCTA	CTTAGTTATA	CAGGCACTGAC	CTGTAAAGACCCCAACATCTAC	3000
Db	2941	CACAAATGTCTA	CTTAGTTATA	CAGGCACTGAC	CTGTAAAGACCCCAACATCTAC	3000
QY	3001	TGAAAAGACACAC	AGCCCTGTGAGAGCA	AGGGGTTGTCTCTGAGC	CTTTGGGTCTTGATGTG	3060
Db	3001	TGAAAAGACACAC	AGCCCTGTGAGAGCA	AGGGGTTGTCTCTGAGC	CTTTGGGTCTTGATGTG	3060
QY	3061	CCACAAAAGAGAGG	CAATGAGTGAATPAA	GGCCCCCAGAGCCTTTAG	AGAGGGCACTTG	3120
Db	3061	CCACAAAAGAGAGG	CAATGAGTGAATPAA	GGCCCCCAGAGCCTTTAG	AGAGGGCACTTG	3120
QY	3121	GGAAAGGGGTCA	GTCTGACAGAGCCCCCTAT	CACTGGAATCTGAGGCCTG	GGGCAACTGTGTG	3180
Db	3121	GGAAAGGGGTCA	GTCTGACAGAGCCCCCTAT	CACTGGAATCTGAGGCCTG	GGGCAACTGTGTG	3180
QY	3181	TAAATCTTGTGGGCTGT	GCACAGCATTTCAAG	CAGACCTGCAATCTCTGTGG	CAGCCTTGGGGA	3240
Db	3181	TAAATCTTGTGGGCTGT	GCACAGCATTTCAAG	CAGACCTGCAATCTCTGTGG	CAGCCTTGGGGA	3240
QY	3241	GGCGGAAAGGAGCAAA	CCCCCACTTAATAC	CTTTTCTCCCTGAGCCCCCAG	ATTAAACACT	3300
Db	3241	GGCGGAAAGGAGCAAA	CCCCCACTTAATAC	CTTTTCTCCCTGAGCCCCCAG	ATTAAACACT	3300
QY	3301	CTGGCTTTC	CCCCCTTCCAC	CTCCCATCAGAGT	GTGACAGAGGAGGT	3360

Dp	3301	CTGCCTTCCCTCCCACTCCCACTGAGAGTGGAGGTTGCAGAGGGGTTAAAA		3360
Qy	3361	CCTACATGTCCTCAACATCATGTGTGCAGATATATGATCAATATGTGTAGAGCAGAAA		3420
Dp	3361	CCTACATGTCCAAACATCATGTGTGCAGATATATGATCAATATGTGTGTAGAGGCAAGAAA		3420
Qy	3421	GGAAATTCGCAGGCTTAACTGGGTTAAATGTGTAAAGTCTGTGTGCATGTGTGTGTCTG		3480
Dp	3421	GGAAATTCGCAGGCTTAACTGGGTTAAATGTGTAAAGTCTGTGTGCATGTGTGTGTCTG		3480
Qy	3481	ACTGAAAAACGGGACATGGCTGTGTGCAGCTGTTCAGTTCGTGTGTGATGAGGTTACACACTGCA		3540
Dp	3481	ACTGAAAAACGGGACATGGCTGTGTGCAGCTGTTCAGTTCGTGTGTGATGAGGTTACACACTGCA		3540
Qy	3541	GGTTTGTGTGTAAATTGCCCAAGGCAAAATGGGATGAAATCCCTTCGAATGTTTAAAGAT		3600
Dp	3541	GGTTTGTGTGTAAATTGCCCAAGGCAAAATGGGATGAAATCCCTTCGAATGTTTAAAGAT		3600
Qy	3601	TGATGTATGGCTGCTCATCTCAAGAACATGTGAAATATGAATGTGACACTCTATATGTGTCT		3660
Dp	3601	TGATGTATGGCTGCTCATCTCAAGAACATGTGAAATATGAATGTGACACTCTATATGTGTCT		3660
Qy	3661	CTAAGCTTAAGGTAGCAAGGTCTTGTGAGAGCACCTGTCTAGAGATGTGGCAACAGAGAC		3720
Dp	3661	CTAAGCTTAAGGTAGCAAGGTCTTGTGAGAGCACCTGTCTAGAGATGTGGCAACAGAGAC		3720
Qy	3721	TACAGACAGTATCTGTACAGATTAAGAGAGAGAGAGAGGGGTGTGAATTTCTTTACTA		3780
Dp	3721	TACAGACAGTATCTGTACAGATTAAGAGAGAGAGAGAGGGGTGTGAATTTCTTTACTA		3780
Qy	3781	TCAAGAGGAAACATGATGTGTGCACCTTGCAAAATGTGATGTCTCTCCCTGACATCATGTACTT		3840
Dp	3781	TCAAGAGGAAACATGATGTGTGCACCTTGCAAAATGTGATGTCTCTCCCTGACATCATGTACTT		3840
Qy	3841	TGTCTCTGGGAGGCACGACCTGTGGAACTTTCAGTCTGTAGAGATGTAGAGGCTCCCTCA		3900
Dp	3841	TGTCTCTGGGAGGCACGACCTGTGGAACTTTCAGTCTGTAGAGATGTAGAGGCTCCCTCA		3900
Qy	3901	GCTTGAAGCTATGCGATAGCCACAGGTTTGAAGGGGGGAAAGGAGAGCCTGGATGTGGAGC		3960
Dp	3901	GCTTGAAGCTATGCGATAGCCACAGGTTTGAAGGGGGGAAAGGAGAGCCTGGATGTGGAGC		3960
Qy	3961	TTTGTGTGTGAGAGGACAGGAGCAATATTTAAGCCTGTGAAGAGAGGTGACCTTATCCAG		4020
Dp	3961	TTTGTGTGTGAGAGGACAGGAGCAATATTTAAGCCTGTGAAGAGAGGTGACCTTATCCAG		4020
Qy	4021	TTTGTTCAACTCACCTTTCAGATTTAAAAATACTGAGTAAAGGCTGTGGGTAGGGAGGTG		4080
Dp	4021	TTTGTTCAACTCACCTTTCAGATTTAAAAATACTGAGTAAAGGCTGTGGGTAGGGAGGTG		4080
Qy	4081	GTGTGAGACGCTCCTGTCTCTCTCTGCATGCTTGAGGCTTGTGGAGAGAGAAATGT		4140
Dp	4081	GTGTGAGACGCTCCTGTCTCTCTCTGTCTCTCTCTGATGAGGCTTGTGGAGAGAGAAATGT		4140
Qy	4141	GCCCAAGGACCTAAAAAAGGAGCCATGTGAGAGCCAGAGGGGGGAGAGGCAACGACTTTCAATGG		4200
Dp	4141	GCCCAAGGACCTAAAAAAGGAGCCATGTGAGAGCCAGAGGGGGGAGAGGCAACGACTTTCAATGG		4200
Qy	4201	GCAAACTTGGGGCCGATAGTATCGATTGCAAGAACTCGCCAAATGATATCCCTTCTTC		4260
Dp	4201	GCAAACTTGGGGCCGATAGTATCGATTGCAAGAACTCGCCAAATGATATCCCTTCTTC		4260
Qy	4261	TTTCTAAGGACAGAGAGGGAATCGAGTTTACCACTCCCTATCACTGATATAGAAAAATGGA		4320
Dp	4261	TTTCTAAGGACAGAGAGGGAATCGAGTTTACCACTCCCTATCACTGATATAGAAAAATGGA		4320
Qy	4321	AAATGCGATTTACACACTCCCTATCATGTGATGTGAGAAAAATGGAAGTGAAGTTTCACTC		4380
Dp	4321	AAATGCGATTTACACACTCCCTATCATGTGATGTGAGAAAAATGGAAGTGAAGTTTCACTC		4380
Qy	4381	CCTATCAGATGATAGAGAAAAAGTGAAGTGAAGTTTACCACTCCCTATCACTGATATAGAAA		4440
Dp	4381	CCTATCAGATGATAGAGAAAAAGTGAAGTGAAGTTTACCACTCCCTATCACTGATATAGAAA		4440

Db	4292	-----	4291
Oy	4441	AAAGTAAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAGTAAAGTCGAGTTTAA	4500
Db	4292	-----	4291
Oy	4501	CCACTCCCTATCAGTGATAGAGAAAGTAAAGTCGAGTTTACCACTCCCTATCAGTGAT	4560
Db	4292	-----	4291
Oy	4561	AGAGAAAAGTAAAGTCGAGCTCCGTTACAGACAGAGACTCCAAATTTAGGACAGAGCA	4620
Db	4292	-----	4291
Oy	4621	TATGGGATGGGATATTAAGGGGCTGGAGCACTGAGAGCTGTCAGAGATTTCTCCAAACCA	4680
Db	4329	TATGGGATGGGATATTAAGGGGCTGGAGCACTGAGAGCTGTCAGAGATTTCTCCAAACCA	4388
Oy	4681	GGTAAGAGGAGTTCCGGTGGGGCTCTTACCCACACACAGACCTCTCCCACTTGAA	4740
Db	4389	GGTAAGAGGAGTTCCGGTGGGGCTCTTACCCACACACAGACCTCTCCCACTTGAA	4448
Oy	4741	GGAAATGCGCTTTCTCTGGAATGGGGTTCAGGCCGTGACAGATCTGACAGGGTGGCTT	4800
Db	4449	GGAAATGCGCTTTCTCTGGAATGGGGTTCAGGCCGTGACAGATCTGACAGGGTGGCTT	4508
Oy	4801	CCACGAGCTGGGAAAGTTCTCAGTGGCAGAGATTTCCACAGAAACACTGGATGCCCT	4860
Db	4509	CCACGAGCTGGGAAAGTTCTCAGTGGCAGAGATTTCCACAGAAACACTGGATGCCCT	4568
Oy	4861	TCCCTTAAGCTGTCTTCTTCATCTTCTCTGGGGATGCTCTCCCGTCTTGGTTATC	4920
Db	4569	TCCCTTAAGCTGTCTTCTTCATCTTCTCTGGGGATGCTCTCCCGTCTTGGTTATC	4628
Oy	4921	TTGGCTCTTGGCTTCAGACAGATTTGGCCCTGTGTGTCACATCTTCTCTACGT	4980
Db	4629	TTGGCTCTTGGCTTCAGACAGATTTGGCCCTGTGTGTCACATCTTCTCTACGT	4688
Oy	4981	CTCGGCTTTGCTTGCCTTCTTGCGTGTCTTTCGACCAACCATTTCTCACTGACC	5040
Db	4689	CTCGGCTTTGCTTGCCTTCTTGCGTGTCTTTCGACCAACCATTTCTCACTGACC	4748
Oy	5041	TTTTCTGCCCTTTCATTTGTAATCATCTTCCTTCCTTCCTTCCTTCCTTCCTTC	5100
Db	4749	TTTTCTGCCCTTTCATTTGTAATCATCTTCCTTCCTTCCTTCCTTCCTTCCTTC	4808
Oy	5101	CTTCCCTTCCTTCTTTCCTCCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC	5160
Db	4809	CTTCCCTTCCTTCTTTCCTCCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC	4868
Oy	5161	CTGTGTCAAGATGCTGAGAAATCACACCTGGGGTTCCACCTTATGTAAACAATCTTCCA	5220
Db	4869	CTGTGTCAAGATGCTGAGAAATCACACCTGGGGTTCCACCTTATGTAAACAATCTTCCA	4928
Oy	5221	GTGAGCCACAGCTTCAGTGTGCTGGGGTCTCTTACCTTCTCACAACCCCTGGCTTGTG	5280
Db	4929	GTGAGCCACAGCTTCAGTGTGCTGGGGTCTCTTACCTTCTCACAACCCCTGGCTTGTG	4988
Oy	5281	CTGTTCATCTCTGGTCAGAGATCTTGAATGATCTCCAGCCTTGTCTCTCTTCTCT	5340
Db	4989	CTGTTCATCTCTGGTCAGAGATCTTGAATGATCTCCAGCCTTGTCTCTCTTCTCT	5048
Oy	5341	GCGGTTCCTCTCTGTGTCAGAGCTGGGCACTGTGATCCTGTTCAGAGCTGTGTCCAC	5400
Db	5049	GCGGTTCCTCTCTGTGTCAGAGCTGGGCACTGTGATCCTGTTCAGAGCTGTGTCCAC	5108
Oy	5401	ATTCTTCAGATTCTCTGAAAAATTACACAGGTGGAATGTTTCCCTGTGAGACAGACA	5460
Db	5109	ATTCTTCAGATTCTCTGAAAAATTACACAGGTGGAATGTTTCCCTGTGAGACAGACA	5168
Oy	5461	TCAGATTTCTCCCGGAAGTCAGAGCTTCAAGCTCTCTTTCTCTGACCAGCTGCCGGCA	5520
Db	5169	TCAGATTTCTCCCGGAAGTCAGAGCTTCTTTTCTCTGACCAGCTGCCGGCA	5228

[illegible][illegible]

QY 301 AGGTTGGGAGAGTGGGGCTTGAGAGAGAGTGGGAGAGTGGCAAAAGCCATCCCTAG 360
DB 301 AGGTTGGGAGAGTGGGGCTTGAGAGAGAGTGGGAGAGTGGCAAAAGCCATCCCTAG 360
QY 361 GGCCTGTGAGATTGGAGCTTTCCTGTACAGCACTGGCTCATAGATCTCTCCAGCC 420
DB 361 GGCCTGTGAGATTGGAGCTTTCCTGTACAGCACTGGCTCATAGATCTCTCCAGCC 420
QY 421 AAACATAGCAAGAGATATCTCTTTGTGATTTCCCAAGGCCAGTACTGTCAAGTT 480
DB 421 AAACATAGCAAGAGATATCTCTTTGTGATTTCCCAAGGCCAGTACTGTCAAGTT 480
QY 481 GAAACAGSATTAGAGAGCCCTGAACTCACTGAATCTGAAGCTCATCCACAGCA 540
DB 481 GAAACAGSATTAGAGAGCCCTGAACTCACTGAATCTGAAGCTCATCCACAGCA 540
QY 541 AGCAGCTAAGGTGCACCTGCTAGTTAGTATCTACGCTGATATATGCAAGCTGGGCCAC 600
DB 541 AGCAGCTAAGGTGCACCTGCTAGTTAGTATCTACGCTGATATATGCAAGCTGGGCCAC 600
QY 601 AGAAGTCTGGGGGTGAGAGACCTGACCACTGATTTTCACTGGCAAAAGGTATGACCCC 660
DB 601 AGAAGTCTGGGGGTGAGAGACCTGACCACTGATTTTCACTGGCAAAAGGTATGACCCC 660
QY 661 TCACAGATAGTAAATGTCCCTTGAATCCATCCAGGCAAGTCTCTAAGAGACATG 720
DB 661 TCACAGATAGTAAATGTCCCTTGAATCCATCCAGGCAAGTCTCTAAGAGACATG 720
QY 721 GGATGAGAGATGATCATGTGGCAATTCACACACAGCTATCCACAGTGTCCCTTGGCCC 780
DB 721 GGATGAGAGATGATCATGTGGCAATTCACACACAGCTATCCACAGTGTCCCTTGGCCC 780
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QY 841 GACACACCCCTGGTGTGAGATTCATTTCTTCAAGTCCCTCTGTGACTTCAT 900
DB 841 GACACACCCCTGGTGTGAGATTCATTTCTTCAAGTCCCTCTGTGACTTCAT 900
QY 901 TTGCAAGGCTTTTTCAGCTGTGACGTGTGGAAGATAGAGTTGGCCTTAGGTGGCAA 960
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DB 961 GGCATCTCAAGAGAAAGCAGACACAGGGGAGACCAATTTTGAAGATACGAACATAA 1020
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DB 1021 TCACGTGGGGGCTGGGGGGTAGAAAAAGAGTAGAGTCCGCTCCAGCTAAGCCAAAG 1080
QY 1081 TAGTCCCGAGATACTCTGACAGCTGGCTGCTCGGGGTAGCTTTAGGAATGTGGTTC 1140
DB 1081 TAGTCCCGAGATACTCTGACAGCTGGCTGCTCGGGGTAGCTTTAGGAATGTGGTTC 1140
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DB 1141 TGAAGACATAGGAGATTGGAAGACATCTTTGAGTCTCCCTCAACCCCACTTACAGAC 1200
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DB 1261 GCAACCAAGACATAGGCGCTGTGCTGAGATGAAGTGTGTTACCAATAGCAAAAACAG 1320
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DB 1321 CAGGGAGGGAGAACAGAGAACGAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
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DB 1381 TGCAGTCAAGAGATGGGAGGCCAACACAGCTTGAAGAGAGAGAGAGAGAGAGAGAG 1440
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OY	4741	GGAAATGCTCTTCGTGAGTGGGGTTCAGAGCCGGTCAGAGATCTGA CAGAGTGCCCT	4800
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OY	4801	CCACCAAGCTTGGGAAGTTCTCAGTGGCAGAGGTTTCCAAAGAAACCTGATGCCCC	4866
Db	4509	CCACCAAGCTTGGGAAGTTCTCAGTGGCAGAGGTTTCCAAAGAAACCTGATGCCCC	4568
OY	4861	TCCCTTAAGCTGTCTTCTCAATCTTCTCCTGAGGATGCTCCTCCCGCTCTTGTTATC	4920
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OY	4921	TTGGCTTTCGTCTTCAGCAAGATTGGCCCTGATGCTGCACTCCATCTTCTCTACTGT	4980
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OY	4981	CTCCGTGCTTGCCTTGGCCTTCTTGCGTGCCTTCCACCACTTCTCACTTCAAC	5040
Db	4689	CTCCGTGCTTGCCTTGGCCTTCTTGCGTGCCTTCTTCCACCACTTCTCACTTCAAC	4748
OY	5041	TTTTCTCCCTTCATATTGTATTCATCCCTTCCTTCCTTCCTTCCTTCCTTC	5100
Db	4749	TTTTCTCCCTTCATATTGTATTCATCCCTTCCTTCCTTCCTTCCTTCCTTC	4808
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OY	5161	CTGTGTCAAGTGTCTGAATCA CACTGAGGTTCCACCCCTAATGTAAACAATTTCCA	5220
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OY	5221	GTGAGCCACAGCTTCAGTGTGCTGTGGTCTCTTACCTTCTCACCCTGCTGTGC	5280
Db	4929	GTGAGCCACAGCTTCAGTGTGCTGTGGTCTCTCTTACCTTCTCACCCTGCTGTGC	4988
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Db	4989	CTGTTCACATCCGTGACAGATCTCAGAAATGTCTCCAGCCTCGATACCTCTTCCT	5048
OY	5341	GCCTGTTCCTCTCTCTGTCTCAGCTGCGCACTGTGATGCTGTCTCAGCTGTGTCCAC	5400
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OY	5401	ATTCTTCAGATTTCTCTGAAAATTAA CAGGTGAAATGTTTCCCTGTATGACAGCAGA	5460
Db	5109	ATTCTTCAGATTTCTCTGAAAATTAA CAGGTGAAATGTTTCCCTGTATGACAGCAGA	5168
OY	5461	TCAGATTTCTCCCGAAGTCAAGGCTTCAGGCTCTCTTCTCTGTCGAGGCGCCGCA	5520
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OY	5521	CTTTTAGCAAACTTCAGGACCCCTTACCCTACATAGACCTTGA CAGAGAAAGGACGACT	5580
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OY	5701	TCCCTTCATCTCCCCCTAAGAGTTTGAAGTGCAC 5735	
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RESULT 3
AC099577 235759 bp DNA linear HTG 22-FEB-2004
LOCUS AC099577
DEFINITION Mus musculus chromosome 14 clone RP23-171A13 map 14, *** SEQUENCING
IN PROGRESS *** 6 unordered pieces.
AC099577
AC099577.3 GI:42734575
KEYWORDS HTG; HTGS PHASE1; HTGS_FULITOP; HTGS_ACTIVEFIN.
ORGANISM Mus musculus
MUS musculus (house mouse)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Birten,B., Nusbbaum,C. and Lander,E.
TITLE Mus musculus chromosome 14, clone RP23-171A13
JOURNAL Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 235759)
Birten,B., Linton,L., Nusbbaum,C., Lander,E., Ali,A., Allen,N.,
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Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
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JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
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AUTHORS 3 (bases 1 to 235759)
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O'Neil,D., Oliver,J., Peterson,K., Phunhthang,P., Pierre,N.,
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Talamas,J., Teefaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
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JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Feb 22, 2004 this sequence version replaced gi:31581779.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://fpc.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR

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REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus

1 (bases 1 to 185702)

Muzny,D,Marle, Metzker,M, Lee, Abramson,S, Adams,C, Alder,J, Allen,C, Allen,H, Alsbrooks,S, Amin,A, Anguiano,D, Anyalebechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H, Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F, Bismalo,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M, Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E, Cardenas,V, Carter,K, Cavazos,I, Ceasar,H, Center,A, Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J, Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L, Davila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D, Delgado,O, Denson,S, Deramo,C, Ding,Y, Dinh,H, Divya,K, Draper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Evans,K, Egan,A, Escotto,M, Eugene,C, Evans,C, Falls,T, Fan,G, Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P, Frazer,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M, Gebregeorgis,E, Geer,K, Gill,R, Grady,M, Guerra,W, Guevara,W, Gunaratne,P, Haaland,W, Hamil,C, Hamilton,C, Hamilton,K, Harvey,T, Havlak,P, Hawes,A, Henderson,N, Hernandez,J, Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M, Hollins,B, Howells,S, Hulik,S, Hume,J, Idlebird,D, Jackson,A, Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A, Karpathy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C, Kowals,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J, Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J, Lorensbuehler,L, Loulsgard,H, Lozada,R,J, Lu,X, Ma,J, Maheshwari,M, Mahindaratne,M, Mahmoud,M, Mallory,K, Mangum,A, Mangum,B, Mapa,P, Martin,K, Martin,R, Martinez,E, Mawhney,S, McLeod,M,P, McNeill,T,Z, Meenen,E, Milosavljevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S, Morgan,M, Morris,K, Morris,S, Mundasa,M, Murphy,M, Nair,L, Nantervis,C, Neal,D, Newton,N, Nguyen,N, Norris,S, Nwaokelemeh,O, Okunolu,G, Olarnpunsagoon,A, Pal,S, Parks,K, Pasternak,S, Paul,H, Perez,A, Perez,L, Pfankoch,C, Plopper,F, Polindexter,A, Popovic,D, Primus,E, Pu,L-L, Puazo,B, Quirroz,J, Rachlin,E, Reeves,K, Regier,M,A, Reich,R, Reilly,B, Reilly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F, Rivers,C, Rodkey,T, Rojas,A, Rose,M, Rose,R, Ritz,S,J, Sanders,M, Saverly,G, Scherer,S, Scott,G, Shattman,S, Shen,H, Shetty,J, Shvartbeyn,A, Sison,I, Sitter,C,D, Smajs,D, Sneed,A, Sodergren,E, Song,X-Z, Sorelle,R, Sosa,J, Steinhilber,M, Strong,R, Sutton,A, Svatek,A, Tabor,P, Taylor,C, Taylor,T, Thomas,N, Thomas,S, Tingey,A, Trejos,Z, Uman,K, Valas,R, Vera,V, Villalana,D, Waldron,L, Walker,B, Wang,J, Wang,Q, Wang,S, Warren,J, Warren,R, Wei,X, White,F, Williams,G, Willson,R, Wlaczek,R, Wooden,H, Morley,K, Wright,D, Wright,R, Wu,J, Yakub,S, Yen,J, Yoon,L, Yoon,V, Yu,F, Zhang,J, Zhou,J, Zhou,X, Zhao,S, Dunn,D, von Niederhausern,A, Weiss,R, Smith,D,R, Holt,R,A, Smith,H,O, Weinstein,G, and Gibbs,R,A.

Direct Submission

Unpublished

2 (bases 1 to 185702)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 185702)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:31195973.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold,

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Unpublished

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individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: KCAL

Center clone name: CH230-249H6

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 158880 bases at least Q40

Consensus quality: 159964 bases at least Q30

Consensus quality: 160601 bases at least Q20

Estimated insert size: 162428; sum-of-contigs estimation

Quality coverage: 9x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 185702; contig of 185702 bp in length.

Location/Qualifiers

1. 185702

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/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-249H6"

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/note="clone_boundary"

clone_end:77

site:

end_sequence:82214368"

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/note="wgs contig"

184218..185702

/note="wgs_contig"

ORIGIN

Query Match 40.9%; Score 2343; DB 2; Length 185702;

Best Local Similarity 71.2%; Pred. No. 0;

Matches 4321; Conservative 0; Mismatches 795; Indels 951; Gaps 55;

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4 GCATCTGACAGTACACACAGGCTCTCCACACAGGCTGCTGCTCAATTGCT 60

5 GCATCTGACAGTACACACAGGCTCTCCACACAGGCTGCTGCTCAATTGCT 60

6 GCATCTGACAGTACACACAGGCTCTCCACACAGGCTGCTGCTCAATTGCT 60

7 GCATCTGACAGTACACACAGGCTCTCCACACAGGCTGCTGCTCAATTGCT 60

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9 GCATCTGACAGTACACACAGGCTCTCCACACAGGCTGCTGCTCAATTGCT 60

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12 GCATCTGACAGTACACACAGGCTCTCCACACAGGCTGCTGCTCAATTGCT 60

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DB 100252 GAGAAAGGAGCTTTGGGAAAGGGGTCACTTGTGACAGGAGCCCTTATCATAGGAATCTGAGGAC 100311
QY 3167 GGGGCAAACTGTGTAAATCTCTGGGCTGCAAGGATTTCAAGAGAGCACTGATCTC 3226
DB 100312 GGGGCAAACTGTGTAAATCTCTGGGCTGCAAGGATTTCAAGGATTTCAAGGATTTCTC 100371
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Db	101449	TGAGAGCTGTCAAGACCGAGATTTTCTCAATCCAGGTATAGAGGAGTTTACGTGGGGCT	101548
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[illegible]

RESULT 5	AC119293/c	AC119293	210784 bp	DNA	linear	HTG_19-NOV-2002
LOCUS		Rattus norvegicus clone	CH230-272D8,	WORKING	DRAFT	SEQUENCE.
DEFINITION		AC119293				
ACCESSION		AC119293.4	GI:25072533			
VERSION		HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.				
KEYWORDS		Rattus norvegicus (Norway rat)				
SOURCE		Rattus norvegicus				
ORGANISM						

REFERENCE
AUTHORS

1 (bases set to 2.0784)
 Muzny,D.,Matie, Metzker,M.,Lee, Abramson, S., Adams C., Alder,J.,
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 Baldwin,D., Bandaranaike,D., Barber,M., Barnesstead,M., Benahmed,F.,
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Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Piazzi, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reih, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, E., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Saverly, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villanueva, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleszyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinrock, G., and Gibbs, R.A.

Unpublished
2 (bases 1 to 210784)
Worley, K.C.

Direct Submission
Submitted (26-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 210784)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23602929.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Project project name: GRM
Center clone name: CH230-272D8

----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 180229 bases at least Q40
Consensus quality: 182328 bases at least Q30
Consensus quality: 183274 bases at least Q20
Estimated insert size: 184593; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 210784: contig of 210784 bp in length.
Location/Qualifiers
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FEATURES
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ORIGIN
Query Match 40.9%; Score 2343; DB 2; Length 210784;
Best Local Similarity 71.2%; Pred. No. 0; Mismatches 795; Indels 951; Gaps 55;
Matches 4321; Conservative 0;

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LOCUS
DEFINITION
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beta-alpha myosin heavy chain intergenic spacer region, complete
sequence; and alpha myosin heavy chain gene, promoter region.
ACCESSION
AY191158
VERSION
AY191158.1 GI:32493126
KEYWORDS
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 5487)
Haddad, F., Bodel, P. W., Qin, A. X., Giger, J. M. and Baldwin, K. M.
Role of Antisense RNA in Coordinating Cardiac Myosin Heavy Chain
Gene Switching
J. Biol. Chem. 278 (39), 37132-37138 (2003)
JOURNAL
PUBMED
2 (bases 1 to 5487)
Haddad, F., Qin, A. X. and Baldwin, K. M.
Direct Submission
Submitted (04-DEC-2002) Physiology and Biophysics, University of
California Irvine, Medical Science 1, D360, Irvine, CA 92697, USA
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DEFINITION AC115371

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Db 2756 AGCCCCAGAGAGGTTAGAGAGGGGTACAGAGTTTACCTGGGAAGGAGAGTGTGCG 2815
Qy 3140 AGCCCTATCTCATGGAATCTGAGCCTGGGGCCAACTGGTGTAAATCTCTGG----- 3191
Db 2816 AGCCCGCAAGTGGAAATTCGAGCCTGGGGCCAAAGGATTAATCTCTGAGCTGCCA 2875
Qy 3192 ----GCTGCCAGGCAATTCAAAGACACCTGCATCTTGGCAGCTGGGGAGGCGGAA 3247
Db 2876 GTCCCCAGCAGCCATCCCAAGCGCACCTGCATCTTGGCAGCCTGGAAAGACGGA 2935
Qy 3248 GGGAGCAACCCCACTTAATCCCTTTCCTCAGCCCCAGATTAACCTCTGGCC-- 3306
Db 2936 GGGAGCAACCCCACTTAACCCCTCTCTCAGCCCCAGATTAACCTCTGGCCCT 2995
Qy 3307 TTCCTCTTCCCACTCCCATCAGAGTGAAGGTTGACAGAGGAGGTTAAAACTTACA 3366
Db 2996 TTCCACCTCTCATCCCACTCAGAGTGAAGGTTTACAGAGGAGGTTAAAACTGTG 3055
Qy 3367 TGTCCAAACATCATGTGTGACATATATGATCATGTGTAGAGCAAGAAAGAAAT 3426
Db 3056 TGTCCAAACATGTGTGTGCA--GATATATGACACAGTACATGTAGACGCAAAAAAGAAAT 3114
Qy 3427 CTGAGGCTTAATCTGGGTATATGTGTAAAGTCT--TGTGTGATGTGTGTGTCTGACTGA 3485
Db 3115 CTCCAGCTTAAGCTGGGTAAATGTGTGAAGCCGTGTGTGTGTGTGTGTGTGTGTGT 3174
Qy 3486 AAGCGGCAATGTGTGTGAGCTGTTCAGTTCTGTGCGTGAAGTTACAGACTCAGAGTT 3545
Db 3175 GTGTGTGTGTGTCT--GCAACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3233
Qy 3546 GTGTGTAAATTTGCCAAGGCAAGT--GGTGAATCTTTCATGTGTTAAAGATTTGA 3604
Db 3234 GTTTGTAAATTTGCCAAGGCAAGTGGGGTGAATCTCCGTTGTAAAGCATTTGA 3293
Qy 3605 TGTATGCTGTGATCTCAAGGACATGGAATTAAGATGACATCTTAATATGTCTCTAA 3664
Db 3294 TGTATGG--CGGCATGTGGGGACAAAT--CAGGTAAAGTAACTCTTAATGTGTCTCCAA 3351
Qy 3665 GCTAAGGTAGCAAGTCTTTGAGAGCACCTGTCTAGAGATGTGGCAACAGAGACTCA 3724
Db 3352 ACCAAGGTAGCAAGGCTTTGAGAGATCTGTCTAGAGACATGTGGCAACAGAGACTCA 3411
Qy 3725 GACAGTATCTGTAACAGATTAAGGAG-----AGAGAGGGGGT 3763
Db 3412 GACAGCATTTATACAGATTAAGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 3471
Qy 3764 GTAGAAATCTCTTAATTAAGAGAACTGATCTGTGCACTGTGCAAAAGTGTCTCTC 3823
Db 3472 AGTAATTTTATTAATTAAGAGAACTGATCTGAACTGTGAACTTAAGTGTCTCTC 3531
Qy 3824 CTTAGACATGATGATCTTGTCTGTGGGAGCCAGACCTGTGAACTTCAAGTCTGAGAG 3883
Db 3532 CTTGAGCATTTTATCTTTGATCTCTGGAGATCTAGCACTGTGAACTTCAAGTCTGAGAG 3591
Qy 3884 GTAGAGGCTCCCTCAGCCTGAGCTTAATGAGATTAAGAGGTTGAAAGGGGAAAGGA 3943
Db 3592 GTAGAGAGATCCCTCAGCCTGAGCTGTGACATTAAGCAGAGAGAGAGAGAGAGAG 3646
Qy 3944 GAGCTTGGATTTGGAGGCTGTGTGTGTGAGAGCAGGAGAGAGATTAAGCTGTGAAGAG 4003
Db 3647 -----GGAGCTGTGATTAAGCTTGAAGCTTGGGATTAAGTATTAGCTGTGAAGAG 3695

QY 4004 AGGTGACCCCTTACCAGT--TGTCAACTCAACCTTGCAGATTAAATAATATGAGGTTAAG 4062
DB 3696 AGGTGACCCCTTACCAGTGTGCTCACTAACCTTGCAGATTAAATAATATGAGGTTAAGG 3755
QY 4063 GC--CTGGGTAGGGAGAGTGTGTGAGACGCTCTGTCTCTCTGTGCAATGCCCTGAGGC 4120
DB 3756 CCAATGTGGGGAAGGAGTGTGTGCTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3815
QY 4121 CTTTGGGGAGAGAGATGTGTGCAAGACTAAAGGCACTAAAGGCAATGAGGCAAGGAGGCA 4180
DB 3816 CTTTGGGGAGAGAGATGTGTGCAAGACTAAAGGCACTAAAGGCAATGAGGCAAGGAGGCA 3875
QY 4181 GGGCAACAGACCTTTTCATGGGCAACCTTGGGGCC 4216
DB 3876 GGGCAACAGACCTTTTCATGGGCAACCTTGGGGCTC 3911

RESULT 9
AR054006 1679 bp DNA linear PAT 29-SEP-1999
LOCUS AR054006 Sequence 11 from patent US 5834306.
DEFINITION AR054006
ACCESSION AR054006
VERSION AR054006.1 GI:5978868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1679)
AUTHORS Webster,K.A. and Bishopric,N.H.
TITLE Tissue specific hypoxia regulated therapeutic constructs
JOURNAL Patent: US 5834306-A 11 10-NOV-1998;
FEATURES
source 1. 1679
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 22.3%; Score 1279.8; DB 6; Length 1679;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 1616; Conservative 0; Mismatches 57; Indels 292; Gaps 1;

QY 3767 GAATTCCTTACTATCAAGGGAAGTGAAGTGTGCAACCTGCAAGTGAAGTGTCTCCCT 3826
DB 1 GAATTCCTTACTATCAAGGGAAGTGAAGTGTGCAACCTGCAAGTGAAGTGTCTCCCT 60
QY 3827 AGACATCATGACTTTGTCTCTGTGGGAGCCAGCACTGTGAACTTCAAGTCTGAGAGATA 3886
DB 61 AGACATCATGACTTTGTCTCTGTGGGAGCCAGCACTGTGAACTTCAAGTCTGAGAGATA 120
QY 3887 GGAAGCTCCCTCAGCCTGAAGCTATGAGATAGCAAGGTTGAAGGGGGAAGGAGAG 3946
DB 121 GGAAGCTCCCTCAGCCTGAAGCTATGAGATAGCAAGGTTGAAGGGGGAAGGAGAG 180
QY 3947 CCGGGATGGGACCTGTGTGTGGAGGAGGAGGAGAGATATTAACCTGGAAGAGAG 4006
DB 181 CCGGGATGGGACCTGTGTGTGGAGGAGGAGGAGAGATATTAACCTGGAAGAGAG 240
QY 4007 TGAACCTTACCCAGTGTGTCACTCAACCTTCAAGATTTAAATAATATGAGGTTAAGG 4066
DB 241 TGAACCTTACCCAGTGTGTGTCACTCAACCTTCAAGATTTAAATAATATGAGGTTAAGG 300
QY 4067 GGGTGAAGGAGTGTGTGTGAGAGCTCTGTCTCTCTCTGCAATGCGGCTTTTG 4126
DB 301 GGGTGAAGGAGTGTGTGTGAGAGCTCTGTCTCTCTCTGCAATGCGGCTTTTG 360
QY 4127 GGGAGAGAGATGTGCAAGGACTAAAGGCACTAAAGGCAATGAGGCAAGGAGGCA 4186
DB 361 GGGAGAGAGATGTGCAAGGACTAAAGGCACTAAAGGCAATGAGGCAAGGAGGCA 420
QY 4187 CAGACCTTTTCATGGGCAACCTTGGGGCCGTAGTATGATGATGACAAGAACTGCAAT 4246
DB 421 CAGACCTTTTCATGGGCAACCTTGGGGCCGTAGTATGATGATGACAAGAACTGCAAT 480

QY 4247 CGATACCTTCTTCTTCTTAAGGAGCAGAGGGAAGTCTGAGTTTACCTCTCTATCAGTG 4306
DB 481 GGAATAAAGAGAGAGAGCAGAGCAGAGGGAAGTGTGAGGAG----- 525
QY 4307 ATAGAGAAAAGTGAAGTGAAGTTTACCACTCTCTATCAGTATAGAGAAAAGTGAAGT 4366
DB 526 ----- 525
QY 4367 CGAGTTTACACTCTCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCACTCTCTA 4426
DB 526 ----- 525
QY 4427 TCAGTATAGAGAAAAGTGAAGTTTACCACTCTCTATCAGTATAGAGAAAAGT 4486
DB 526 ----- 525
QY 4487 GAAAGTCAGTTTACCACTCTCTATCAGTATAGAGAAAAGTGAAGTGAAGTTTACCACT 4546
DB 526 ----- 525
QY 4547 TCCTATCAGTATAGAGAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 4606
DB 526 ----- 525
QY 4607 TTAGGACAGAGCATATGAGATGAGATTTAAAGGGGCTGAGACTGAGAGCTGTGACAG 4666
DB 549 TTAGGACAGAGCATATGAGATGAGATTTAAAGGGGCTGAGACTGAGAGCTGTGACAG 608
QY 4667 ATTTCTCCAAACCCAGTAAAGAGGAGTTTGGGTTGGGGGCTTTTACCAACCAAGAGCT 4726
DB 609 ATTTCTCCAAACCCAGTAAAGAGGAGTTTGGGTTGGGGGCTTTTACCAACCAAGAGCT 668
QY 4727 CTCCCACTAGAGAAAAGTCTCTCTGAGAGTGGGGTTCAAGCCGCTGAGAGATCT 4786
DB 669 CTCCCACTAGAGAAAAGTCTCTCTGAGAGTGGGGTTCAAGCCGCTGAGAGATCT 728
QY 4787 GACAGAGTGGCTTTCAACAGCTTGGGAAATTTCTAGTGTGAGAGAGTTTCCAAAGAAA 4846
DB 729 GACAGAGTGGCTTTCAACAGCTTGGGAAATTTCTAGTGTGAGAGAGTTTCCAAAGAAA 788
QY 4847 CACTGAGTGGCTTCCCTTACAGTGTCTTCCATCTTCTCCCTGGGGATGCTCTCTCC 4906
DB 789 CACTGAGTGGCTTCCCTTACAGTGTCTTCCATCTTCTCCCTGGGGATGCTCTCTCC 848
QY 4907 CGTCTGAGTTATCTTGTGCTCTTGTGCTTGTGCAAGAAATTTGCGCTGTGTCACTCA 4966
DB 849 CGTCTGAGTTATCTTGTGCTCTTGTGCTTGTGCAAGAAATTTGCGCTGTGTCACTCA 908
QY 4967 TCTTTCTCTACTGTCTCGGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 5026
DB 909 TCTTTCTCTACTGTCTCGGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 968
QY 5027 TTTTCACCTTACCTTTTCTCCCTTCAATTGATTCATGCTCTCTCTCTCTCTCTCTCT 5086
DB 969 TTTTCACCTTACCTTTTCTCCCTTCAATTGATTCATGCTCTCTCTCTCTCTCTCTCT 1028
QY 5087 TCTTCT 5146
DB 1029 TCTTCT 1088
QY 5147 TCTTCT 5206
DB 1089 TCTTCT 1148
QY 5207 TAAACATCTTCAAGTGAAGCAGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5266
DB 1149 TAAACATCTTCAAGTGAAGCAGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1208
QY 5267 CCGCTGAGCTGTCTGTGTCACTCTGATCAGAGATCTTGAATGATCTTCCAGCTCTG 5326
DB 1209 CCGCTGAGCTGTCTGTGTCACTCTGATCAGAGATCTTGAATGATCTTCCAGCTCTG 1268

Oy	5327	TTACTCCCTCTCCGCGCGTTCCTCTCTGTGACAGCGCGGCACTGGAGGAGCCCTGTTG	5386
Db	1289	CTACTCTCTTCTCCGCTGTTCCTCTCTGTGACAGCTGGCGCACTGGAGGAGCCCTGTTG	1328
Oy	5387	CAGCTGTGATCCACATTTCTTCAGGATTTCTGTGAAAAGTTAAACAGGTAGATGTTTCCC	5446
Db	1329	CAGCTGTGATCCACATTTCTTCAGGATTTCTGTGAAAAGTTAAACAGGTAGATGTTTCCC	1388
Oy	5447	CTGTAGACAGACGATCAAGATTCTTCCGGAAAGTCAGGCTTCCAGGCCCTCTCTTCTGTGC	5506
Db	1389	CTGTAGACAGACGATCAAGATTCTTCCGGAAAGTCAGGCTTCCAGGCCCTCTCTTCTGTGC	1448
Oy	5507	CCAGCTGCCCGGCACTCTTAGAAACCTCAGGCACTTACCCCATAGAACCTCTGCA	5566
Db	1449	CCAGCTGCCCGGCACTCTTAGAAACCTCAGGCACTTACCCCATAGAACCTCTCTGCA	1508
Oy	5567	GAGAAAGCAGGCACTTACATGAGTCTGTGGGAGAGCCATAGGCTACGGTGTAAAGA	5626
Db	1509	GAGAAAGCAGGCACTTACATGAGTCTGTGGGAGAGCCATAGGCTACGGTGTAAAGA	1568
Oy	5627	GGCAGGGAAGTGTGTGTAGGAAAAGTCAGACTTCACATAGAACCTTAGCCACACAG	5686
Db	1569	GGCAGGGAAGTGTGTGTAGGAAAAGTCAGACTTCACATAGAACCTTAGCCACACAG	1628
Oy	5687	AAATGACAGACGATCCCTCCATCTTCCCCCTAAGATTGTAAGT 5731	
Db	1629	AAATGACAGACGATCCCTCCATCTTCCCCCTAAGATTGTAAGT 1673	

RESULT 10				
AR146182				
LOCUS	AR146182	1679 bp	DNA	linear
DEFINITION	Sequence 11 from patent US 6218179.			PAT 08-AUG-2001
ACCESSION	AR146182			
VERSION	AR146182.1			
KEYWORDS	GI:15109371			
SOURCE	.			
ORGANISM	Unknown.			
REFERENCE	Unknown.			
AUTHORS	1 (bases 1 to 1679)			
	Webster,K.A., Bishopric,N.H., Murphy,B., Laderoute,K.R. and			
	Green,C.J.			
TITLE	Tissue specific hypoxia regulated constructs			
JOURNAL	Patent: US 6218179-A 11 17-APR-2001;			
FEATURES	Location/Qualifiers			
source	1..1679			
	/Organism="unknown"			
	/mol_type="unassigned DNA"			
ORIGIN				

Query Match	22.3%	Score 1279.8	DB 6	Length 1679
Best Local Similarity	82.2%	Pred. No. 0		
Matches 1616	Conservative 0	Mismatches 57	Indels 292	Gaps 1
QY	3767	GAATTCTCTTACTATCAAAAGGAAA	CTGAGTCGTGACCTGCAAAAGTGATGCTCTCCCT	3822
Db	1	GAAATCTCTTACTATCAAAAGGAAA	CTGAGTCGTGACCTGCAAAAGTGATGCTCTCCCT	60
QY	3827	AGACATCATGACTTTGTCTCTGGGAGG	CAGCAGCTGTGAACTTACAGGCTCAGAGAGTA	3886
Db	61	AGACATCATGACTTTGTCTCTGGGAGG	CCAGCAGCTGTGAACTTACAGGCTCAGAGAGTA	120
QY	3887	GGAGGCTCCCTCCTGAGCTGAAAGTATG	CAGATAGCCAGGCTTGAAAAGGGGAAAGGAGAG	3946
Db	121	GGAGGCTCCCTCCTGAGCTGAAAGTATG	CAGATAGCCAGGCTTGAAAAGGGGAAAGGAGAG	180
QY	3947	CCTGGATGAGGAGCTGTGTGTGTGGAGG	CAGAGGGAACAGATATTAAGCTCTGAAGAGAAAG	4006
Db	181	CCTGGATGAGGAGCTGTGTGTGTGGAGG	CAGAGGGAACAGATATTAAGCTCTGAAGAGAAAG	240
QY	4007	TCACCTTACCAAGTTGTTGAACTCAC	CTTCAGATTTAAAAATACTAGGTAAGGGCTT	4066
Db	241	TCACCTTACCAAGTTGTTGAACTCAC	CTTCAGATTTAAAAATACTAGGTAAGGGCTT	300

[illegible]

QY	5147	CCCTTCCTTCCTTCCTGTCAGAGTGTGAGATTCACACCTGGGGGTTCCACGCTTATG	5206
Db	1089	TCTCTTCCTTCCTTCCTGTGTGAGAGTGTGAGAAATCACACTGGGGTTCCACGCTTATG	1148
QY	5207	TAAACAAATCTTTCAGTGAAGCCACAGCTTCAGTGTGTGTGGGTGTCTTTACCTTCTCA	5266
Db	1149	TAAACAAATCTTTCAGTGAAGCCACAGCTTCAGTGTGTGTGGGTGTCTTTACCTTCTCA	1208
QY	5267	CCCCCTGGCTTGTCTCTGTTCATCTCTGTGATGAGATCTTAAATTGTCTCCAGCTCTG	5326
Db	1209	CCCCCTGGCTTGTCTCTGTTCATCTCTGTGATGAGATCTTAAATTGTCTCCAGCTCTG	1268
QY	5327	CTACTCCCTCTCCTGCGCTGTCTCTCTCTGTGACAGTGGGCACTGTGGAGCCCTGTG	5386
Db	1269	CTACTCCCTCTCTCTGCTGCTGTCTCTCTGTGACAGTGGGCACTGTGGAGCCCTGTG	1328
QY	5387	CAGCTGTGTGTCCAGATCTTCAGGAATCTCTGAAAAGTTTAAACGAGTGAATGTTC	5446
Db	1329	CAGCTGTGTGTCCAGATCTTCAGGAATCTCTGAAAAGTTTAAACGAGTGAATGTTC	1388
QY	5447	CTGTAGACAGCAGATTCACGATTTCTCCGGGAAGTCAAGGCTTCAGGCTCTCTTCTCTGC	5506
Db	1389	CTGTAGACAGCAGATTCACGATTTCTCCGGGAAGTCAAGGCTTCAGGCTCTCTTCTCTGC	1448
QY	5507	CCAGCTGCGCGGCACTCTTAGCAAACTCAGGCAACCTTAGCCCAATAGACCTCTGACA	5566
Db	1449	CCAGCTGCGCGGCACTCTTAGCAAACTCAGGCAACCTTAGCCCAATAGACCTCTGACA	1508
QY	5567	GAGAAAGCAGCACTTTATCATGAGTCTGTGTGGAGAGCCATAGGCTTACGGTGTAAAGA	5626
Db	1509	GAGAAAGCAGCACTTTATCATGAGTCTGTGTGGAGAGCCATAGGCTTACGGTGTAAAGA	1568
QY	5627	GGCAGGGGAAGTGTGTGTGTAGAAAAGTCAGACCTTCACATAGAAAGCTTAGCCACACAG	5686
Db	1569	GGCAGGGGAAGTGTGTGTGTGTAGAAAAGTCAGACCTTCACATAGAAAGCTTAGCCACACAG	1628
QY	5687	AAATGACAGACAGATCCCTCTATCTCCGCCAATAAGATTTGAAT	5731
Db	1629	AAATGACAGACAGATCCCTCTATCTCCGCCAATAAGATTTGAAT	1673

RESULT	11
AX546496	
LOCUS	AX546496 1679 bp DNA linear PAT 26-NOV-2002
DEFINITION	Sequence 5 from Patent WO0249669.
ACCESSION	AX546496
VERSION	AX546496.1 GI:25811663
KEYWORDS	.
SOURCE	Mus sp.
ORGANISM	Mus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Schn,C.A., Padua,R., Bonner,M., Donovan,M.G. and Soykan,O. Electrically responsive promoter system Patent: WO 0249669-A 5 27-JUN-2002; Medtronic, Inc. (US)
FEATURES	location/Qualifiers 1..1679 /organism="Mus sp." /mol_type="unassigned DNA" /db_xref="taxon:10095"

	Query Match	22.3%	Score 1279.8	DB 6	Length 1679
	Best Local Similarity	82.2%	Pred. No. 0		
	Matches 1616	Conservative	0	Mismatches 57	Indels 232
				Gaps	1
OY	3767	GAATTCCTCTTACTATCAAGGAAACTGATGTCGCACTGCGAAAGTGGAGCTCTCCCT	3828		
Db	1	GAATTCCTTATCAACAAAGGAAACTGATGTCGCACTGCGAAAGTGGAGCTCTCCCT	60		
OY	3827	AGACATCATGACTTTGTCTCTGGGAGGACGACACTGTGGAACCTTCAGGTCTGAGAGACTA	3886		

Db	61	AGACATCATATACCTTTGTCTCTGGGGAGCCAGCACTGTGGAACCTTCAGGTCTGAGAGGT	120
Qy	3887	GGAGGCTCCCTCAAGCTTAAGCTATGCAATAGCCAGGTTGAAGGGGAAAGGAG	3946
Db	121	GGAGGCTCCCTCAAGCTTAAGCTATGCAATAGCCAGGTTGAAGGGGAAAGGAG	180
Qy	3947	CTGCGATGGGACCTGTGTGTGTGGAGGCGAGGGGACGATATTAAGCTGGAAGAGAAG	4006
Db	181	CTGCGATGGGACCTGTGTGTGTGGAGGCGAGGGGACGATATTAAGCTGGAAGAGAAG	240
Qy	4007	TGACCCCTTACCAGTGTTCATCTCACTCACTTCAGATTTAAATTAATGAGSTAAAGGCT	4066
Db	241	TGACCCCTTACCAGTGTTCATCTCACTTCAGATTTAAATTAATGAGSTAAAGGCT	300
Qy	4067	GGGTAGGGGAGTGTGTGTGAGACGCTCTGTCTCTCTGCAATGCCTTGAGGCCCTTTG	4126
Db	301	GGGTAGGGGAGTGTGTGTGAGACGCTCTGTCTCTCTGCAATGCCCTTTG	360
Qy	4127	GGGAGAGGAATGTGCCCAAGACTAAAAAAGGCCATGAGCCAGAGGGGCGAGGCA	4186
Db	361	GGGAGAGGAATGTGCCCAAGACTAAAAAAGGCCATGAGCCAGAGGGGCGAGGCA	420
Qy	4187	CAGACCTTTATGGGCAAACTTGGGGCCGGTATGATTCATTTGACAAAGAACTGCCAAT	4246
Db	421	CAGACCTTTATGGGCAAACTTGGGGCCGGTATGATTCATTTGACAAAGAACTGCCAAT	480
Qy	4247	CGATACCTTCTTCTTCTTAACGACAGAGAGGAATCGATTTAACCACTCCATCAGTG	4306
Db	481	GGATCAAAAGAGAGGAGGACGAGGACGAGAGGAAAGTGGAGGGAG-----	525
Qy	4307	ATAGAGAAAAGTGAAGTCGAGTTTACCACTCCCTATCAGTATAGAAAAAGTGAAGT	4366
Db	526	-----	525
Qy	4367	CGAGTTTACCACTCCCTATCAGTATAGAAAAAGTGAAGTGAAGTTTACCACTCCCTA	4426
Db	526	-----	525
Qy	4427	TCAGTGTATAGAAAAAGTGAAGTCGAGTTTACCACTCCCTATCAGTATAGAAAAAGT	4486
Db	526	-----	525
Qy	4487	GAAAGTCGAGTTTACCACTCCCTATCAGTATAGAAAAAGTGAAGTGAAGTTTACCACT	4546
Db	526	-----	525
Qy	4547	TCCTTATCAGTATAGAAAAAGTGAAGTCGAGCTCGGTACCAAGAGAGACTTCCAAT	4606
Db	526	-----GGTCCAGCGAGAGACTCCAAT	548
Qy	4607	TTAGGCGAGCGACTTATGGATGGGATATATAAGGGGCTGGAGCACTAGAGCTTCCAG	4666
Db	549	TTAGGCGAGCGACTTATGGATGGGATATATAAGGGGCTGGAGCACTAGAGCTTCCAG	608
Qy	4667	ATTTCCTCAAACCAAGTAAAGGAGATTTGGGTGGGGGCTCTTCAACCAACCAAGACT	4726
Db	609	ATTTCCTCAAACCAAGTAAAGGAGATTTGGGTGGGGGCTCTTCAACCAACCAAGACT	668
Qy	4727	CTGCCCACTTAAGAAAGAACTGCTTTCTCTGGAAGTGGGTTCAAGGCCGTCAGAGATCT	4786
Db	669	CTGCCCACTTAAGAAAGAACTGCTTTCTCTGGAAGTGGGTTCAAGGCCGTCAGAGATCT	728
Qy	4787	GACAGGATGGCTTCCACAGAGCTGGGAGTTCTCAGTGGCAGAGAGTTTCCAAAGAA	4846
Db	729	GACAGGATGGCTTCCACAGAGCTGGGAGTTTCTCAGTGGCAGAGAGTTTCCAAAGAA	788
Qy	4847	CAGTGAATGCCCTTCCCTTACGCTGTCTTCTCATTTCTCTCTGGGGAATGCTCTCC	4906
Db	789	CAGTGAATGCCCTTCCCTTACGCTGTCTTCTCATTTCTCTCTGGGGAATGCTCTCC	848
Qy	4907	CGTCTTGTTTATCTTGGCTTCTGTCTTACGAAAGTTTGCCTGTGTCTCCACTCCA	4966

Db	849	CGTCTGGATTATCTTGAGCTCTTGCTCTTACAGACAAGATTGGCCCTGTCGTCCACTTCA	908
Oy	4967	TCCTTCTCTACTGTCTCCGTCGCTTGCCTTGCCTTCTGTGCGGTGTCCTTCTTCCACCCA	5026
Db	909	TCCTTCTCTACTGTCTCCGTCGCTTGCCTTGCCTTCTGTGCGGTGTCCTTCTTCCACCCA	968
Oy	5027	TTTCTCACTTCAACCTTTCTCCCTTCTGCATTTTGTATTACCTTCTCTTCTTCTTCT	5086
Db	969	TTTCTCACTTCAACCTTTCTCCCTTCTGCATTTTGTATTACCTTCTCTTCTTCTTCT	1028
Oy	5087	TCCTTCT	5146
Db	1029	TCCTTCT	1088
Oy	5147	TCCTTCT	5206
Db	1089	TCCTTCT	1148
Oy	5207	TAAACATCTTCCAGTAGACCAACGCTTCACTGCTGCTGGTGTCTTACCTTCTCTCA	5266
Db	1149	TAAACATCTTCCAGTAGACCAACGCTTCACTGCTGCTGGTGTCTTACCTTCTCTCA	1208
Oy	5267	CCCCCTGGCTTGTCTCTGTTCATCTCTGTGACAGATCTCTAATTGTCTCCACGCTCTG	5326
Db	1209	CCCCCTGGCTTGTCTCTGTTCATCTCTGTGACAGATCTCTAATTGTCTCCACGCTCTG	1268
Oy	5327	CTACTCCCTCTCTCTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	5386
Db	1269	CTACTCCCTCTCTCTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1328
Oy	5387	CAGCTGTGTCTCAACTTCTTACAGATTCTCTGAAAAGTTAAACAGGTGAGATGTTTCC	5446
Db	1329	CAGCTGTGTCTCAACTTCTTACAGATTCTCTGAAAAGTTAAACAGGTGAGATGTTTCC	1388
Oy	5447	CTGTAGACAGACATCAAGATTCTCCGGGAAGTACAGGCTTCCAGCCCTCTTCTCTGCG	5506
Db	1389	CTGTAGACAGACATCAAGATTCTCCGGGAAGTACAGGCTTCCAGCCCTCTTCTCTGCG	1448
Oy	5507	CCAGCTGCCCGGCACTCTTACGAAACCTCAGGCACTTACCCCAATAGACCTCTGACA	5566
Db	1449	CCAGCTGCCCGGCACTCTTACGAAACCTCAGGCACTTACCCCAATAGACCTCTGACA	1508
Oy	5567	GAGAAAGCAGGCACTTACATGAGTCTCTGTGGAGAGCCATAGGCTACGGTGTAAAAGA	5626
Db	1509	GAGAAAGCAGGCACTTACATGAGTCTCTGTGGAGAGCCATAGGCTACGGTGTAAAAGA	1568
Oy	5627	GGCAGGGAGTGTGTGTGTAGAAAGTCAAGACTTCAATAGAAAGCTCAGCCACACAG	5686
Db	1569	GGCAGGGAGTGTGTGTGTAGAAAGTCAAGACTTCAATAGAAAGCTCAGCCACACAG	1628
Oy	5687	AAATGACAGACAGATCCCTCCATCTTCCGCCATAAGAGTTTGAGT	5731
Db	1629	AAATGACAGACAGATCCCTCCATCTTCCGCCATAAGAGTTTGAGT	1673
RESULT 12			
MUSCHMG			
MUSCHMG			
LOCUS	MUSCHMG	2594 bp	DNA linear ROD 27-APR-1993
DEFINITION	Mus musculus cardiac myosin heavy chain gene, 5' end.		
VERSION	M62404.1	GI:192609	
KEYWORDS	cardiac myosin heavy chain.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Guilick,J., Subramaniam,A., Neumann,J. and Robbins,J.		
TITLE	Isolation and characterization of the mouse cardiac myosin heavy chain gene		
JOURNAL	J. Biol. Chem.	266 (14), 9180-9185	(1991)
MEDLINE	91225025		
PUBMED	2026617		

COMMENT	Original	source	text: Mus musculus DNA.
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	/db_xref="taxon:10090"		
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intron	624..1304		
	/number=1		
exon	1305..1373		
	/number=2		
intron	1374..1664		
	/number=2		
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intron	1881..>2594		
	/number=3		
ORIGIN			
Query Match	22.3%;	Score 1279.8;	DB 10; Length 2594;
Best Local Similarity	82.2%;	Pred. No. 0;	
Matches 1616; Conservative	0;	Mismatches 57;	Indels 292; Gaps 1;
QY	3767	GAATTCTCTTAATCAATCAAAAGGAACTGAGTCGTGCACCTCCGAAAGTGGATGCTCTCCCT	3826
DB	1	GAATTCCTCTAATCAAAAGGAACTGAGTCGTGCACCTCCGAAAGTGGATGCTCTCCCT	60
QY	3827	AGACATCATGACTTGTCTCTGGGAGCAGACATGTGGAATTCAGGCTCGAGAGACTA	3886
DB	61	AGACATCATGACTTGTCTCTGGGAGCAGACATGTGGAATTCAGGCTCGAGAGACTA	120
QY	3887	GGAGGCTCCCTCAGCCTGAACTATGCGATGACCAAGGCTTGAAGGGGAGAGGAGAG	3946
DB	121	GGAGGCTCCCTCAGCCTGAACTATGCGATGACCAAGGCTTGAAGGGGAGAGGAGAG	180
QY	3947	CCTGGGATGGAGCTTGTGTGTGGAGCGAGCGAGATTTAAGCTCGAAGAGAGAG	4006
DB	181	CCTGGGATGGAGCTTGTGTGTGGAGCGAGCGAGATTTAAGCTCGAAGAGAGAG	240
QY	4007	TGACCCCTTACCAAGTTGTCAACCACTCAGATTAAATATACAGGTAAGGGGCT	4066
DB	241	TGACCCCTTACCAAGTTGTCAACCTCAGATTAAATATACAGGTAAGGGGCT	300
QY	4067	GGGTAGGGAGGTGTGTGAGACGCTCCTGTCTCTCTCTGTCATGCCCCCTGAGGCCCTTTG	4126
DB	301	GGGTAGGGAGGTGTGTGAGACGCTCCTGTCTCTCTCTCTGTCATGCCCCCTGAGGCCCTTTG	360
QY	4127	GGGAGGAGGAATGTGCCCAAGACTAATAAAAAAGCCATGAGACCCAGAGGCGCTA	4186
DB	361	GGGAGGAGGAATGTGCCCAAGACTAATAAAAAAGCCATGAGAGCCAGAGGCGCAA	420
QY	4187	CAGACCTTCAATGGCAAACTTGGGGGCCGTAAGATGATGATGAACAAGACTGGCAAT	4246
DB	421	CAGACCTTCAATGGCAAACTTGGGGGCCCTGTGTCTCTGTCACTCCAGAGCCAG	480
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DB	526	-----	525


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QY 4367 CGAGTTTACCACTCCCTATCAGTATAGAGAAAAAGTGAAGTGAAGTTTACCACTCCCTA 4426
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QY 4487 GAAAGTCGAGTTTACCACTCCCTATCAGTATAGAGAAAAAGTGAAGTGAAGTTTACCACT 4546
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QY 5147 TCTTCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5206
Db 1089 TCTTCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1148
QY 5207 TAAACAATCTTCCAGAGACCAAGCTTCAAGTCTGAGTCTGAGTCTTCTTCTTCTTCTTCTA 5266
Db 1149 TAAACAATCTTCCAGAGACCAAGCTTCAAGTCTGAGTCTGAGTCTTCTTCTTCTTCTA 1208
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Db 1209 CCCCCTGAGCTGCTGCTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1268
QY 5327 CTACTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5386
Db 1269 CTACTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1328
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Db 1329 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1388
QY 5447 CTGTAGACAGACAGATCAGATTTCTCCGGAAGTCAAGCTTCCAGCCCTCTTCTTCTCTGC 5506

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Db 1389 CTGTAGACAGACAGATCAGATTTCTCCGGAAGTCAAGCTTCCAGCCCTCTTCTCTGC 1448
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Db 1449 CCAGCTGCCCGGCACTCTTACGAAACCTCAGGACCTTTACCCCATATAGACTCTTGACA 1508
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Db 1509 GAGAAGCAGGACCTTATAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1568
QY 5627 GGCAGGGAAGTGTGTGTAGAGAAAGTCAAGACTTCAATAGAAAGCTTACCCACAGCAG 5686
Db 1569 GGCAGGGAAGTGTGTGTAGAGAAAGTCAAGACTTCAATAGAAAGCTTACCCACAGCAG 1628
QY 5687 AATATACAGACAGATCCTCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5731
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RESULT 13
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LOCUS Human chromosome 14 DNA sequence BAC C-2201G16 of library Caltech-D
DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL132855
VERSION AL132855.4 GI:13897280
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Molecular data: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157910)
Heilig, R., Picot, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,
Brothier, P., Catolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Crnaud, C.,
Gyapay, G., Saurin, W. and Weissenbach, J.
Sequencing of the human chromosome 14
Unpublished
2 (bases 1 to 157910)
Genoscope.
Direct Submission
Submitted (26-APR-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
On Apr 30, 2001 this sequence version replaced gi:12001727.
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: segref@genoscope.cns.fr
-----
The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-124D2
Downstream BAC (overlapping the SP6 end) : R-66N24 (AC=AL135991)
----- Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 6.97x in Q20 bases; sum-of-contigs
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Overall quality chart :
Range : bases
0 - 9 : 26
1 - 9 : 8
10 - 19 : 58
20 - 29 : 115
30 - 39 : 574
40 - 49 : 4774
50 - 59 : 7043
60 - 69 : 9171
70 - 79 : 24066
80 - 89 : 56139
90 - 99 : 55936

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Percentage of bases with a quality value >= 40 : 99 %.
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    /db_xref="taxon:9606"
    /chromosome="14"
    /clone_lib="C-2201G16"
    /clone_1ib="Caltech-D"
    13550..13694
    /note="matching EMBL:AA452257
    RHD:RH92419
    dbSTS:STS65422
    Identified using the e-PCR software (G. Schuler)"
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    RHD:RH76320
    dbSTS:STS53407
    Identified using the e-PCR software (G. Schuler)"
    57409..57527
    /note="matching EMBL:X52889
    RHD:RH96140
    dbSTS:STS7881
    Identified using the e-PCR software (G. Schuler)"

STS
Query Match 9.7%; Score 558.2; DB 9; Length 157910;
Best Local Similarity 63.7%; Pred. No. 3,4e-164;
Matches 1380; Conservative 0; Mismatches 658; Indels 127; Gaps 30;

ORIGIN
Query Match 9.7%; Score 558.2; DB 9; Length 157910;
Best Local Similarity 63.7%; Pred. No. 3,4e-164;
Matches 1380; Conservative 0; Mismatches 658; Indels 127; Gaps 30;
2096 CTCACCTGTGCGCAGAGCGTTCATCTGTGTCAACATCTCTAGAAATGTCAGACTGC 2155
44522 CTCACCTGTGCGCAGAGCGTTCATCTGTGTCAACATCTCTAGAAATGTCAGACTGC 44463
QY 2156 AGGGCT-----GCTTGGAGAGCAGCTGGAAGATGTGTAGAGCCAGGGAGACA 2207
DB 44462 GGAAGCTGTGTGCAAGCTTGAAGGAGAGCGGAGACCAATATGTAGAGCAGGAGAGA 44403
QY 2208 AGGGGGCTTGAAGAGAGAGAGGAGGCAACAGGCGCACAAAGAGGAGAGCCAGA 2267
DB 44402 A-GGAGCTTGGAGAGAGAGAGAGGAGGAGGAGGAGAGAGC-----GGGAGGGCTTGGG 44348
QY 2268 ACTGAGTTAACTCTTCTCTTGTTCATCTTCATAGAGAGCAGTGGAACTTGTGACCA 2327
DB 44347 GCTGAGTGAACACTTCTCTCTCTCTCTCCACAGAGAGGGGAGACTACCCCCACAC 44288
QY 2328 CCATCCCCCATG-----AGCCCCCATGCCCATACCAAGTTTGGCTGTAGTGCATTCT 2381
DB 44287 CTCACATCCCCGCTGCCCTGACACCACTATACCAAGTGAAGGCTGTCTAGAGACA 44228
QY 2382 AGGTTCCCTGAGAGCAGAGCTGAGCTTTGTCTTGTGAGCTGAGCCCAAGTGAACCAAT 2441
DB 44227 GGGTTCCCTGAGAGCAGAGCTGAGCTTTGTCTTGTGAGCTGAGCCCAAGTGAACCTG 44168
QY 2442 GTTCTCAGTACCTTGTGAATGCTTCAAGAGCTTGAAGACAGGAGTGAATATTAGGCC 2501
DB 44167 GTTCTCAGTACCTTGTGAATGCTTCAAGAGCTTGAAGACAGGAGTGAATATTAGGCC 44109
QY 2502 ATGGGCTTAACTCTGAGCTTGAACAGAGAGCTTCAAGTGAACCTTCAAGGAGACAGCTGC 2561
DB 44108 ATGGGCTTAACTCTGAGCTTGAATGCTTGAAGAGCTTCAAGTGAACCTT-----AGAGCTGG 44057
QY 2562 AGACAGGAGCTTATCCCAAGAGCAACATTTGGCATAGGTGGCTG---AAATGG 2618
DB 44056 GGAAGAGGAGCTTATCCCTGGGGGTAAATGATTTGGCATAGCACTTGAAGAAATGG 43997
QY 2619 GAATGCAAGTTGAATCAGTCTCTTCAAGATATCTGATGACAGACCTTGAAGACCTCTGG 2678
DB 43996 GGAATGTCAGTCACTAAGTCTCTTCAAGACATTTG---AGAAAAGTCTCAAAATGCTCTGG 43938
QY 2679 AGAAGGGGATGTCTCTGCTCCCAACCAACATTAAGGAGAGTGAATATCTTGAAGGGGCT 2738

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DB 43937 AAAGAGAGGTGTCTCTGAGCCCA-----GGAATGGGTGGAGCGCTCTAAGGAGCT 43884
QY 2739 GGCAGACTTGGGAGACACACATTTACTGAGAGTCTGAGCCAGAAAATCTAGCGGCC 2798
DB 43883 AAGG-----GAGAGCCACATCTTATGAAAGTGTCTCTTACCCAGAGAGCTGACCTCT 43829
QY 2799 TGTGTCTTGGCCCACTTCCACACTTGAAGCTATATTGAGAGTGAACATGATTAAGGTGG 2858
DB 43828 GTGTCTTACCACTTCCACACTTGAAGCTATATTGAGAGTGAACATGATTAAGGTGG 43769
QY 2859 GAGCTGTGACGAGGAGAGTGTCTCTGAGTGAAGGAGTGAAGGAGGAGGAGGAGGAGG 2918
DB 43768 ---AGGGGGCTGGAGAGGAGTGTCTCTGAGTGAAGGAGTGAAGGAGGAGGAGGAGG 43713
QY 2919 GAGTGTGCTTGTGTCTCTGAAACAGATGTCTTACTTATGTTATTAACAGCATGACCTGCTA 2978
DB 43712 GAGTGTGCTTGTGTGTCTTCTGAAACAGATGTCTTACTTATGTTATTAACAGCATGAC 43653
QY 2979 AAGACCCAACTATACAGACTTCTGAAAGACAGAGCCCTGAGAGA---CAGGGTTGT 3034
DB 43652 AAGACCTGACACTTACAGCTCTG---AGAGATGAGCAGCATTTGAGAGATGGGAGCGGGGCC 43594
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DB 43593 TTGAGGGCTTGAAGGTGTGTGAGGACACCCGCAAGAGAG---GAATGTGATTTAAGGCC 43537
QY 3095 CCAGAGC-----GTTAGAGAGGCGCACTTGGAGAGGCGTCACTGCAAGAGGCC 3144
DB 43536 TGAAGGCTTGGAGAGGCGCAAAATTTCTGCTGGGAGAGGGGCGAGGTGCGAGAGGCC 43477
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QY 3203 ATTCAAGAGACCTGATCTCTGTGAGCGCTGGGAGAGCGGAGAGGAGCAACCCCA 3262
DB 43418 -----GACCTGACCTCTGTGAGCCCGGTGAGAGAGAGAGAGAGAGCCCTCA 43369
QY 3263 CTATATCCCTTCTCTCTGAGCCCGAGATTAAACATCTTGGCTTCCCTTCCACCT 3322
DB 43368 CCAACCCCTCTCTCTCTGAGCCCTTGAAGATTAGCAGCATCTTCTT-----CTGCCACCC 43313
QY 3323 CCAATGAGAGTGAAGGCTTTCAGAGAGGAGGTTAAACCTTACATCTCCAAACATCATGG 3382
DB 43312 CACCCGAGAGAGAGAGGATGAG-AGGAGGCGCAAAAGCTTATGTGTGCAAAAGCGAGT 43254
QY 3383 TGCAGATATATGATCAGATGTGTGAAGCA---AGAAAAGAAATCTGACAGCTTAAAC 3439
DB 43253 TGCA-AATGTGTGATCTCATGTACAAAGAAAGTGAAGAAATCTGCAAGCTTGAAG 43195
QY 3440 TGGATTATGTGAATGATCTGTGTGATGTGTGTGTGTGTGACTGAAAACGGGCATGGCT 3499
DB 43194 TGGATTATGTGAATGATCTGTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 43143
QY 3500 GTGACAGCTTTCAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3559
DB 43142 -----TCAAGCTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 43093
QY 3560 CAAGCAAGTGGGTGAATCCCTTCATGAGTTTAAAGATTTGATGATGAGCTGATCT 3619
DB 43092 CTGAGGGGCGAGGAGAAATCATCTGCAATTCGTGAGCAGAGTTGAGATGTGTGACACTAT 43033
QY 3620 CAAGCAATGAGAAAATGAATGAGCACTTATATGTGTCTTAAGCTAAGTAG---CA 3676
DB 43032 C-AGAGACATTAAGAGAGGGGTGGAGCTTCAAGCTGTCCCAACAGAGGTGGCTCA 42974
QY 3677 AGGTCTTTGAGAGACCTGTCTTGAAGTGTGGGCAAGAGCTACAGACATATCTGT 3736
DB 42973 AGACTTGGAGAACTTGTCTGAAGACTTGGGGAACAG-----AAGGAGACAGGAGCAT 42919
QY 3737 ACAGATTAAGGAGAGAGAGGAGGAGTGAATTTCTTACTATCAAGAGAACTGAG 3796

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Db      42918 GGCATTATGACAGTGAAGCCAGACAGA-----ATTTCCTGACAAAAAAACTGAG 42865
Qy      3797 TCGTGACCTCGAAAGTGAATGCTCTCCCTAGACATCATGACTTGTCTCTGGGGAGCCA 3856
Db      42864 CCATGGAGATGACACAGATCCCTTCCTGGGACCAT-ACGCAAGCTTTTATGTCCTTA 42806
Qy      3857 GCACTGTGAACCTTCAGTCTGAGAGTGAAGAGCTCCCTCAGCCTGAAGCTATGACAG 3916
Db      42805 GCACGTGGGGCTCCAGTACTTAACAGCAGAAAGATGCTCCAGCCTGGAGCTGTGTAGAGG 42746
Qy      3917 ATAGCCAGGTTAAAGGGGAAAGGAGAGCTGGAGATGGAGCTTGTGTGTGAAGCA 3976
Db      42745 AGGTCAAGATGGAGAGAGAGCTGGGAAACAGGGAGAAAGCCATGGTTGGAGAGG 42686
Qy      3977 GGGGACAGATATTAAGCTGGAGAGAGAGAGTGAAGCTTACCAGTGTCAATCAGCCCT 4036
Db      42685 GAGGACAGGCAATTTGGCTGACAGAGAGAGTGAAGCTCACCAGATGTTTCAATCAGCCCT 42626
Qy      4037 TCAGATTTAAATACTGAGTGAAGGCG-----CTGGGTAGGGAGAGTGTGAAGCGC 4091
Db      42625 TCGGCTTAAATAATGAGTGAAGGCGCATGAGAGGCTGGAGAGGCGGTGTGAAGAG 42566
Qy      4092 TCGTGTCTCTCTCTGTCATGAGGCGCTTTGGGAGAGAGAAATGTGCCCAAGACT 4151
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Qy      4152 AAAAAAAGGCGATGAGAGCGGAGAGGCGGAGAGCAAGACTTTCATGGGCAAACTTGG 4211
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RESULT 14
CNS0000B/c      196292 bp      DNA      linear      PRI 22-MAY-2001
LOCUS      Human chromosome 14 DNA sequence BAC R-124D2 of library RRC1-11
DEFINITION      From chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION      AL049829
VERSION      AL049829.4      GI:8217859
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Heilwig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
AUTHORS      Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
      1 (bases 1 to 196292)
      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
      Brothier,P., Catolicco,L., Barbe,V., Pelletier,E., Artiguenave,F.,
      Levy,M., Beckenberg,R., Bruls,T., deBeraudinis,V., Cruaud,C.,
      Gyapay,G., Saurin,W. and Weissenbach,J.
      Sequencing of the human chromosome 14
      Unpublished
      2 (bases 1 to 196292)
      Genoscope.
      Direct Submission
      Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage :
      BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
      - Web : www.genoscope.cns.fr)
      On Jun 3, 2000 this sequence version replaced gi:6138746.
      ----- Genom Center
      Center: Genoscope / Centre National de Sequencage
      Center code: GS
      Web site: http://www.genoscope.cns.fr/
      Contact: SeqRef@genoscope.cns.fr

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TITLE      The following BAC sequence is oriented from the T7 to the SP6 end.
JOURNAL      Upstream BAC (overlapping the T7 end) : R-244B17
AUTHORS      Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC=AL132855)
REFERENCE      ----- Summary Statistics
      Assembly program: Phrap; version 2.0
      Quality coverage: 7.94x in Q20 bases; sum-of-contigs

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Overall quality chart :
Range : bases
1 - 9 :
10 - 19 :
20 - 29 :
30 - 39 :
40 - 49 :
50 - 59 :
60 - 69 :
70 - 79 :
80 - 89 :
90 - 99 :
Percentage of bases with a quality value >= 40 : 99 %.
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dbSTS:STS69699
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Dd	2256	CTCACCTGTGGCCGAGCGCTCCATCTCCGTCTTATATTTCAGAGCTCCGACGAGATGA	2315		
Qy	2156	AGGCGTGGCTTGGGAGGCACTGGAAAGATATGTGAGAGCCAGGGGAGACAAAGGGGCC	2215		
Dd	2316	GGAGCTGTG-TGCAGAGCGCTTTAGGAGAGGACGAGACCAATATCTGAGACAGGAGAG	2374		

QY	2216	TAGAAAG-GAAGAAAGGCAAAACAGCCCAACAAGGGCAGAGCCGAACTAGT	2274
Db	2375	AAGAGCCTGGGGAAGGAGAGCGTACAGCGGCAACGGCAGGGCTGGGCTGAGT	2434
QY	2275	TAACTCCTTCCTGTGTGCATCTTCCATAGAGGAGCGTGGAACTCTGTGACCACCATCC	2334
Db	2435	GAACACTTCCTTCCTTCCTTCCTTCACAGAGAGCGGGGGAGCTAACCCCAACCTCCACTC	2494
QY	2335	CCATGAGCCC-----CCACTACCCTATCCAGATTGGCTGTAGTGGCATTTAGTTCCC	2389
Db	2495	CCGCTGCCCTTCGACACCACTATACCAATGAGGCTCTCTGAGACACAGGGTCCC	2554
QY	2390	TGAGAGACAGAGCTGGCCTTTGTCTCTTGGACCTGACCTGACCAGCTGACCCAACTGTTCTAG	2449
Db	2555	TGAGAGCAAAAGCCTGGTCTTTGTCACTGACCTGACCCCAACCACTGACCTGGGCGTTCTCAG	2614
QY	2450	TACCTTGAATGCCCTCAAGAGCTTGAGAACAGGCGAGTGACATTTAGGCCATGGGCTA	2509
Db	2615	CTCCTTATCATGTCCCCAGAGCTATGGGAACCAACAGTGAAGCAGCT--GGCCATGGGCTA	2673
QY	2510	ACCCTGAGCTTGCAACAGAGAGCCTCAAGTACCTCCAGGGACACAGCTGACACAGGT	2569
Db	2674	ACCCCCGGCTGAATTTCTGGGGCCTCGAGTAACCT-----AGACTGGGGACAGGT	2725
QY	2570	GGCCTTATCCCAAAAGACCAACATTTGGCATAGGTGGCTGC-----AAATGGGAATGCA	2626
Db	2726	GGCGTGATCCC--TGGGGTAAATGATTTGGCATTAAGACCTGCAAGAAATGGGGATGTGG	2784
QY	2627	GGTTGAATCAGGTCCCTTCAAGATATCTGCATGCAAGACTTAAGACCCCTGAGAGAGG	2686
Db	2785	GGTCACTAAGGGTCCCTCCAGAGCACTTG--ACAAAAAGTCCAAATGCTCTGGAAAAGAG	2843
QY	2687	GTATGCTCCGAGCCCAACACCATTAAGGGAGTGAACATCTAGGGGGCTGGCACT	2746
Db	2844	GTGTGTTCTGAGCCCA-----GGAATGGGGTGGCAGCGTCTTAGGAGCTAAGG----	2894
QY	2747	TGGGAGACACCACTTACTGAGAGTGTGAGCCCGAAAAACTGACCGCCTGTGTCT	2806
Db	2895	-GAGAGGCCACATCTTAAATGAAAGGCTCTTAACCAAGAGAGCTGACCCCTGTGTCTCT	2953
QY	2807	GCCCACTCCACACTTAGAGCATATTTAGAGAGTGAACGTGATAGGGTGGAGCTGCT	2866
Db	2954	ACCACTTCCACACCTCGAGCATATTTAGAGAGTGAACGTAACTG---GTGGAGGGG	3010
QY	2867	AGCAGGAGAGTGTTCCTGGGTGTGAGGTTGAAGGGAAGCCAGAGCAGGGAGTCTGG	2926
Db	3011	GGCTGGGAGGGTGTTCCTGGGTGTGAGGTTG--GGGGAAAGGCCAAGCAGGGAGTCTGG	3069
QY	2927	CTTTGTCTCCTGAACAATGTCTACTTAGTTATTAACAGGCATGACCTGTCTTAAAGACCA	2986
Db	3070	CTTGTGTTCTGGAACAATGTCTCACTTAGTATTAACAGGAACAGCCTGTGAAAGCTGG	3129
QY	2987	ACATCTACGACCTCTGAAAAAGACAGAGCCCTGAGAGACAGGGGTTGTCTCTGAGCCTTG	3046
Db	3130	ACACCTTACAGCCTCTG--AGAGATGAGCAGCATTTGAGAGATGGGAGCGGGGCTTGAAGGC	3188
QY	3047	GGTCTTGAATGTGTCCAAAGAGAGGCGCATGAGTGTAGATTAAGGCCCCAGAGC----	3102
Db	3189	TAGGGTCTTGAAGACCAACAAGAAAGGAGATGTGATTAACCTCTGAGAGGGCTTGG	3248
QY	3103	-----GTTAGAAAGGGCACTTTGGGAAGGGTCAAGTCTGCAAGGCCCTTATCAATGAA	3156
Db	3249	AAAAGGGCAACAAATTTCTGCTCTGGGGAAGGGGCAAGTGCAGAGGCCCAACCCCAATGAA	3308
QY	3157	TCTGAGACCTTGGGG--CCAACTGGTGTAAATCTCTGGGCTCTGCAAGCATTTCAAAACAGCA	3215
Db	3309	TGCAGTGCTGGGGAACAATGTGTAAATTCCTCCAGGCTGCAAG-----GCA	3356
QY	3216	CCTGCATCTCTTGGCAGCCTTGGGGAAGCGGAAAGGAGCAACCCCACTTATACCTTTTC	3275
Db	3357	CTGCACCTCTCTGGCAGCCCGGTGAAGCAAGAGGACAGGCCCTTACCAACCCCTCTCT	3416


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Qy 3276 TCCCTAGCCCCAGATTAAACACTCTGGCTTCCCTTCCCACTCCCATCAGAGTG 3335
Db 3417 CTTCAGGCTTGAATGACACACTTCTT-----CTGCCACCCCACCGAGACA 3471
Qy 3336 GAGGTTGCAAGAGGAGTAAACCTACATGTCCAAACATCATGTGCACGATATATG 3395
Db 3472 GAGGTAGCAG--GGAGGGGAAAGCTTATGTGCAAAATGCGGATGTGA--AATGTG 3529
Qy 3396 GATCAGTATGTAGAGCA--AGAAAGAAATCTGCAGCTTAACTGGGTTAATGTGT 3452
Db 3530 CATCCATGTACAAAAGAAAGTAGAAAGAAATCTGCAAGCTTGAGTGGTAAGTGA 3589
Qy 3453 AAGTCATGTGATGATGTGTGTCTGACTGAAAACGGGCATGGCTGTGACGTGTCA 3512
Db 3590 AAAATCTGATGTGTGCTGAATGAGACAGACAGGTCAAG----- 3633
Qy 3513 GTTCTGTGCTGAGTTACCACTGCAGGTTTGTGTAAATTTGCCAAGCAAGTG 3572
Db 3634 --TCTGATGTAGAGTGTCTGAACCTGGGTTCTGTGAAAATCTGCTGAGGCGGACAG 3691
Qy 3573 GTGAATCCCTTCCATGTTTAAAGATTGATGATGGCTGCATCTCAAGACCATGA 3632
Db 3692 GAGAACTACTGCTTGCAGTGTGATGATGTTGGCCACTATTC--AGGACATTAG 3750
Qy 3633 AAATGAAATGACACTTATATGTGTCTTAAGTAAAGTAG--CAAGTCTTTGGAG 3689
Db 3751 GGAAGGGGTGGGACTTCAGACGTGTCCAAACAGGGTGGCTCAAGACTTGGAGA 3810
Qy 3690 ACACTGTCTAGAGATGTGGCAACAGAGACTACAGACATCTGTACAGATAAGAG 3749
Db 3811 ACACTTGTCTGAAGACTTGGGAAACG-----AAGGAGACAGGCATGGCACTTATGCA 3865
Qy 3750 AGAGAGAGGGGTGTGAATTTCTTACTATCAAGGAACTGATGTGCACTGCA 3809
Db 3866 ACTGAGGCCAGACAGAA-----TTTCTGACAAAAGAAACTGAGCCATGAGATGA 3919
Qy 3810 AAGTGAATGCTCCCTAGACATCATGACTTTGTCTGGGGAGCCAGCACTGTGAACT 3869
Db 3920 CAACAGATCTTCCCTGGGCA--CATCTGCAGCTTTTATGCTTAGCACTTGGGGCTC 3977
Qy 3870 TCAGTCTGAGAGTAGAGAGCTCCCTCAGCCTGAAGCTATGCAATAGCCAGGTTG 3929
Db 3978 CAGTACTTAACAGAGAGAAATGCTCCAGCTTGGGACTGTGTAGAGGATGTCAGAATG 4037
Qy 3930 AANAG--GGAGAGGAGACCTGGGATGGAGCTTGTGTGGAGCAAGGACAGATAT 3988
Db 4038 AAGGAGAGGCTGGGAAACAGGGAGAAAGCCATGTGTGGAGGCGGAGACAGCAT 4097
Qy 3989 TAAGCCTGGAAGAGAGTGAACCTTAAACCAAGTTGTCACTCAACCTTCAGATTAAAA 4048
Db 4098 TTGGCTTGAGAGAGATGACCTCAACCATGTTC--AGTCTCACTTGGGGGAAAAA 4156
Qy 4049 TAACTAGGTAAAGGC-----CTGGTAGGGAGTGTGTGACGCTCTGTCTCC 4103
Db 4157 TAACTGAGGTAAAGGCATGGCAGGGTGGAGGGGTGTGAGAAAGTCTGTCTTCC 4216
Qy 4104 TC--TGACGTCCCTGAGGCTTTTGGGAGGAG--AATGTCCCAAGACTAAAAAAG 4160
Db 4217 ACATATCTGTCTCATCAGCCCTTTGAAGGGGAGGTAAATGTGCTTAAAGAAAG 4276
Qy 4161 GCATGAGCCAGAGGGGCGAGGCAACAGACTTTTCATGGGCAAACTTGGGGGCC 4216
Db 4277 CCGTGAAGCCAGAGAGGCTGGGGCAGACCTTTCTTGGGCAAAATCAGGGGGCC 4332
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